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Dd	61	CTCTGTGTCCTCGAGCCAAAGTGTTGTGGGGCCTCGGGTCAAGTTGGAGATCCTG	120			
Qy	121	TCCATCGAGAACCTGAACGGGGAGCTGCAGAACGGGAACCTGCTCGCGCGGCCCGCGAAC	180			
Dd	121	TCCATCGAGAACCTGAACGGGGAGCTGCAGAACGGGAACCTGCTCGCGCGGCCCGCGAAC	180			
Qy	181	CCGGGAGACCGCAAGTGCACC CGCGACGAGTGTGACACATACTTCAAAGTGTGCTCAAG	240			
Dd	181	CCGGGAGACCGCAAGTGCACC CGCGACGAGTGTGACACATACTTCAAAGTGTGCTCAAG	240			

QY	241	GAGTATCAGTCCCGCGTCACGSCGGGGGCGCTGCGAGCTTCGGCTCAGGGTCCAGCCT	300	QY	1321	GGCTGATGGGTGAGCAATAATTTAATGATGCTTGGCCAGTGTCAAGAT	1380
DB	241	GAGTATCAGTCCCGCGTCACGSCGGGGGCGCTGCGAGCTTCGGCTCAGGGTCCAGCCT	300	DB	1321	GGCTGATGGGTGAGCAATAATTTAATGATGCTTGGCCAGTGTCAAGAT	1380
QY	301	GTCAATCGGGGGCAACACTTTCAACCTCAAGCCGAGCGCGCGCAACGACCCGCAATC	360	QY	1381	GACGCTCTCTGTGCGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGGCTATGCA	1440
DB	301	GTCAATCGGGGGCAACACTTTCAACCTCAAGCCGAGCGCGCGCAACGACCCGCAATC	360	DB	1381	GACGCTCTCTGTGCGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGGCTATGCA	1440
QY	361	GTGCTGCTTTTCAGTTTCGCTGGCGAGGTCTCTATACGTTGCTTGTGTGAGGGGTGGAT	420	QY	1441	GGCGATCACTGTGAGAGAGACATCGATGAATGTCAGCAAAACCCCTGTTTGAATGGGGT	1500
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DB	781	TACTGTGATAGTGCATCCACACCCGGGATGCGTCCAGGCACTCTGTAATGAGCCCTGG	840	DB	1861	TTCAACGGGAACTACTGCCATGAAATATTTAATGACTGTGAGAGCAACCCCTGTGAGAAC	1920
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QY	961	CAGTGTCTGCTGAGGGGTATTCAGGACCCCACTGTGAAATTTGCTGAGCACCGCCTGC	1020	QY	2041	ACGTGTCCGACCTGGTCAATGACTTCTACTGTGACTGTAAAAATGGGTGGAAAGAAAG	2100
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QY	1021	CTCTCTGATCCCTGTCAACAGAGGAGCTGTGAAGGAGCTCCCTGGGCTTTGAGTGT	1080	QY	2101	ACCTGCCACTCACGTGACGTGTGATGAGGCCACGTGCAACAAACCGTGGCACCTGC	2160
DB	1021	CTCTCTGATCCCTGTCAACAGAGGAGCTGTGAAGGAGCTCCCTGGGCTTTGAGTGT	1080	DB	2101	ACCTGCCACTCACGTGACGTGTGATGAGGCCACGTGCAACAAACCGTGGCACCTGC	2160
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LOCUS AR136524
DEFINITION Sequence 1 from patent US 6136952.
ACCESSION AR136524
VERSION AR136524.1 GI:14477196
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5590)
AUTHORS Li, L. and Hood, L.
TITLE Human jagged polypeptide, encoding nucleic acids and methods of use
JOURNAL Patent: US 6136952-A 1 24-OCT-2000;
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Db 474 CTCTGTGCTCCCTGCGAGCAAGTGTGTGGGGCTCTCGGGTCAGTTCGAGTTGGAGATCCTG 533
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VERSION CO881401.1 GI:54034369  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Champion, B.R. and Ragno, S.  
TITLE Modulators of the notch signaling pathway immobilized on particles  
for modifying immune responses  
JOURNAL Patent: WO 2004083372-A 95 30-SEP-2004;  
Lorantis Limited (GB)  
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## ORIGIN

Query Match 99.9%; Score 3654.2; DB 6; Length 5590;  
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ACCESSION AR482321  
VERSION AR482321.1 GI:47244642  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 5590)  
Li, L., Hood, L., Krantz, I.D. and Spinner, N.B.  
AUTHORS Methods of diagnosing alagille syndrome  
TITLE Patent: US 6703198-A 1 09-MAR-2004  
JOURNAL The University of Washington and The Children's Hospital of Philadelphia; Seattle, WA  
FEATURES  
source Location/Qualifiers  
1. 5590  
/organism="unknown"  
/mol\_type="mRNA"  
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Query Match 99.98; Score 3654.2; DB 6; Length 5590;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 3653; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
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Db 534 TCCATGACAGAACTGAAACGGGAGCTGACAAACGGGAACTGCTGCGGCGCGCCCGGAAAC 593  
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[illegible]

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VERSION CQ873974.1 GI:52747566
KEYWORDS
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SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE

AUTHORS

Taira, K. and Kawasaki, H.

TITLE

Regulation of mammalian cells

JOURNAL

Patent: WO 2004076622-A 393 10-SEP-2004;

National Institute of Advanced Industrial Science and Technology (JP)

FEATURES

Location/Qualifiers

source

1. 5896

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ORIGIN

Query Match 99.9%; Score 3654.2; DB 6; Length 5896;  
Best local similarity 99.9%; Pred. No. 0;  
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DEFINITION Sequence 13 from Patent EP1471075.
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VERSION CQ894703.1 GI:55467452
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Rosenthal,A.D., Pilarsky,C., Dahl,E., Specht,T., Bruemendorf,T.,
Lichtner,R., Staub,E., Roepcke,S. and Li,X.I.
TITLE Human nucleic acid sequences expressed in pancreatic carcinomas
JOURNAL Patent: Ep 1471075-A 13 27-OCT-2004;
Hinzmann, Bernd (DE); Rosenthal, Andre (DE); Pilarsky, Christian
(DE); Dahl, Edgar (DE); Specht, Thomas (DE); Lichtner, Rosemarie
(DE)
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Db 534 TCCATGCAGAACGTCGAACCGGGAGCTGCAGAACGGGAACCTGTCGCGCGCGCCCGGAAC 593
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Qy 241 GAGTATCAGTCCCGCTCAGCGCGCGGGGCGCTTCGAGCTTCGAGTTCGAGGTCCACGGCT 300
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Db	1734	GGCTGGATGGGTGAGAAATTTGAGACATAAATATTAATGACTGCTTGGCCAGGTGTCAGAAAT	1793
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VERSION CQ981309.1 GI:58190568  
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ORGANISM Homo sapiens  
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Homnidae; Homo.

REFERENCE 1  
AUTHORS Rosenthal, A., Hermann, K., Heiden, E., Pilarsky, C., Bruemendorf, T.,  
Staub, E., Roepcke, S., Mennerich, D., Kinnemann, H. and Li, X.  
TITLE Human nucleic acid sequences from lung tumours  
JOURNAL Patent: EP 1498424-A 164 19-JAN-2005;  
Hanzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esmeralda (DE);  
Rosenthal, Andre (DE)  
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 REFERENCE 1  
 AUTHORS Garcia,T., roman Roman,S., Baron,R., Call,K., Theillhaber,J., Connolly,T., Jackson,A., Bushnell,S.E. and Rawadi,G.



TITLE		Genes involved in osteogenesis, and methods of use	
JOURNAL		Patent: WO 02081745-A 160 17-Oct-2002;	
FEATURES		Aventis Pharma S.A. (FR)	
source		Location/Qualifiers	
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		/note="Homo sapiens jagged 1 (Alagille syndrome) (JAG1)"	
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Best Local Similarity		99.9%; Pred. No. 0;	
Matches 3653; Conservative 3; Mismatches 1; Indels 0; Gaps 0;			
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Qy	61	CTCTGTGCTTCGAGCAAGGTGTGTGGGCTCTGGGTCTGATTCGATTTGGAGATCCTG	120
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Qy	121	TCCATGCAGAACGTGAACGGGAGCTGCAGAACGGGAACCTGCTGGCGGGCGCCCGAAC	180
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Qy	181	CCGGAGACCGCAAGTGCACCCGCGAGAGTGTGACACATCTTCAAAGTGTGCTCAAG	240
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Qy	301	GTCAATCGGGGCAACACTTCAACTCAAGCCAGCGCGGCAACGCGCAACCCGATC	360
Db	714	GTCAATCGGGGCAACACTTCAACTCAAGCCAGCGCGGCAACGCGCAACCCGATC	773
Qy	361	GTGCTGCTTTCAAGTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	420
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Qy	481	ATCAACCCAGCGGAGTGGAGACCTGACAGCAACGCGGCGTTCGCCACTTTGAG	540
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Qy	601	CGCCCCAGAGATGACTTTTGGACACTATGCTCTGTGACAGAAATGGCAACAAACTTGC	660
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Qy	781	TACTGTGATTAAGTGCATCCACACCCGGGATGCGTCCAGCGCATCTGTAAATGAGCCCTGG	840
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Qy	901	GGGACTCATCAGCGGTGTCTCAACGGGGGAACCTTGTAGCAACACAGAGCCCTTGACAAATAT	960
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Qy	961	CAGTGTCTCTGCTGAGGGGTATTTAGGACCCCACTGTGAAATTTGTGAGCAGCGCTGC	1020
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Qy	1021	CTCTCTGATCCCTGTCAACACAGAGCAGCTGTAAAGAGACCTCTCTCTGGGCTTTGAGTGT	1080
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Db	1554	AATAACTGTTTCCACAGGGGACCTGTCAGGACCTGTTTAAACGGATTTAAGTGTGTGTC	1613
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Db	1734	GGTGTGATGGGTGAGAAATTTGTGACATAAATATTAATGAATGCTGCTTGGCCAGTGTCAAGT	1793
Qy	1381	GAGCCCTCTGTCGGGATTTGGTTAATGTTATCGCTGTATCTGTCACCTGGCTATGCA	1440
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Qy	1501	CACGTGCAGATGAATCAACAGATTCAGTGTCTGTGTCCCACTGGTCTCTCTGGAAC	1560
Db	1914	CACGTGCAGATGAATCAACAGATTCAGTGTCTGTGTCCCACTGGTCTCTCTGGAAC	1973
Qy	1561	CTCTGTGAGTGCATCGATTTATGAGCCCTAAATCCCTGCCAGAACGGTGGCCAGTGC	1620
Db	1974	CTCTGTGAGTGCATCGATTTATGAGCCCTAAATCCCTGCCAGAACGGTGGCCAGTGC	2033
Qy	1621	TACAAACCGTCCAGTGAATTTCTGCAAGTCCCGAGGACTATGAGGGCAAGAACTGC	1680
Db	2034	TACAAACCGTCCAGTGAATTTCTGCAAGTCCCGAGGACTATGAGGGCAAGAACTGC	2093
Qy	1681	TACAACTGAAAGACCACTGCGCAAGACCCCTGTGTAAGTGAATGACAGTGCACAGTG	1740
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Db	2154	GCCATGGCTTCCAAACCAACACCTGAAGGGGTGGGTATATTTCTCCACAGCTGTGGT	2213
Qy	1801	CCTTCAGGGAAGTGAAGAGTCACTGGGAGGCAAAATTCACCTGTGACTGTAAACAAAGGC	1860
Db	2214	CCTTCAGGGAAGTGAAGAGTCACTGGGAGGCAAAATTCACCTGTGACTGTAAACAAAGGC	2273
Qy	1861	TTTCAACGGGAACATACTGCCATGAAATAATTAATGACTGTGAGAGCAACCCCTGTAGAAC	1920
Db	2274	TTTCAACGGGAACATACTGCCATGAAATAATTAATGACTGTGAGAGCAACCCCTGTAGAAC	2333
Qy	1921	GGTGGCACTTGCATCCATGGTGTCACTCTCAAGTGCATCTGTAGTGCAGCTGGAG	1980
Db	2334	GGTGGCACTTGCATCCATGGTGTCACTCTCAAGTGCATCTGTAGTGCAGCTGGAG	2393

Qy	1981	GGGGCTTACTGTGAAACCAAATATTAATGACTGAGCCAGAACCCCTGECACAATATGGGGC	2040
Db	2394		
		GGGGCTTACTGTGAAACCAAATATTAATGACTGAGCCAGAACCCCTGECACAATATGGGGC	2453
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Db	2454		
		ACGTGTGCGACCTGGTCAATGACTTCTACTGTGACTGTAAAAATGGGTGGAAGAAAG	2513
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Qy	2161	TATGATGAGGGGATGCTTTTAAAGTGCAATGTGCTTGGCGGCTGGGAAGGAAACAACTGT	2220
Db	2574		
		TATGATGAGGGGATGCTTTTAAAGTGCAATGTGCTTGGCGGCTGGGAAGGAAACAACTGT	2633
Qy	2221	AACATAGCCGGAACAGTAGCTGCTGCCAAACCCCTGCCATTAATGGGGGACATGTGTG	2280
Db	2634		
		AACATAGCCGGAACAGTAGCTGCTGCCAAACCCCTGCCATTAATGGGGGACATGTGTG	2693
Qy	2281	GTCAACGGCGAGTCTCTTTACGTGCGTCTGCAAGGAAGGCTGGAGGGGGCCATCTGTGCT	2340
Db	2694		
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Qy	2341	CAGAATACCAATGACTCGACGCCCTCATCCCTGTTTAAACAGCGGCACTCTGTGGATGGA	2400
Db	2754		
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Db	2994		
		AGACCTTGCATCACCATGGGGAGTGATACCAAGATGGGCCCAATGGGATGATGACTGT	3053
Qy	2641	AATACCTGCCAGTGCCTGAATGAGCGGATCGCCTGTCTCAAAGGTCTGGTGTGGCCCTCGA	2700
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Db	3114		
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Db	3414		
		GCTTGCAGGCTTCCCCTTCCAGCGAACAAATGAAATACATGTGGCAATTTCTGTGAAGAT	3473

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Db	3474	ATACGGGATGATGGGAAACCCGATCAAGGAAATCACTGACAAATAATCGATCTTGTTAGT			
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Db	3534	AAACGTGATGGAACACAGCTCGCTGATTGCTGCGTGTTCGAGAGTAAAGATTACAGAGCGG			3593
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Db	3654	TGGATCTGTTGCTTGGTGACGGCTTCTACTGTGCTTCGCGAAGCGCGGAGAGCCGGC			3713
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ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 4208)				
AUTHORS	Sakano, S. and Itoh, A.				
TITLE	Differentiation-suppressive polypeptide				
JOURNAL	Patent: US 6337387-A 10 08-JAN-2002;				
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Best Local Similarity	99.8%;	Pred. No. 0;			
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Db	409	ATGGCTTCCCCACGGACG	CGCGCGGTTCGGGGCCCGCCCTTAAGCCCTCTGCTCGCCCTG	468	
Qy	61	CTGTGTCCTTCGGAGCC	CAAGTGTGTGGGCGCTCGGGTCAGTTCGAGTTGAGATCCTG	120	
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## RESULT 12

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LOCUS  
DEFINITION  
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AF028593  
AF028593.1 GI:2599081

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

Lindsell, C.E., Shawber, C.J., Boulter, J. and Weinmaster, G.

Jagged: a mammalian ligand that activates Notch1

Cell 80 (6), 909-917 (1995)

7697721

2 (bases 1 to 5457)

Bash, J., Zong, W.X., Banga, S., Rivera, A., Ballard, D.W., Ron, Y. and

Gelinas, C.

Rel/NF-kappaB can trigger the Notch signaling pathway by inducing

the expression of Jagged1, a ligand for Notch receptors

EMBO J. 18 (10), 2803-2811 (1999)

10329626

3 (bases 1 to 5457)

Bash, J., Zong, W.-X. and Gelinas, C.

Direct Submission

Submitted (03-OCT-1997) Center for Advanced Biotechnology and

Medicine, Department of Biochemistry, Robert Wood Johnson Medical

School, University of Medicine and Dentistry of New Jersey, 679

Hoes Lane, Piscataway, NJ 08854, USA

Location/Qualifiers

source

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/db\_xref="taxon:9606"

/chromosome="20"

/map="20p12"

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264. 3920

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/notes="similar to H. sapiens Jagged 1 encoded by GenBank

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/db\_xref="GI:2599082"

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ORIGIN

Query Match 99.9%; Score 3651; DB 8; Length 5457;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3651; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db	384	TCCATGAGAACGTGAACGGGAGCTGCAGAACGGGAACTGTCTGGCGCGCGCCCGGAAC 443
Qy	181	CCGGGAGACCGAAGTGACCCCGAGAGTGTGACATACATCTCAAGGTGTCCTCAAG 240
Db	444	CCGGGAGACCGAAGTGACCCCGAGAGTGTGACATACATCTCAAGGTGTCCTCAAG 503
Qy	241	GAGTATCAGTCCCGCGTCAAGCGCGGGGGCCCTGACAGCTTCGGCTCAGGGTCCAGCCCT 300
Db	504	GAGTATCAGTCCCGCGTCAAGCGCGGGGGCCCTGACAGCTTCGGCTCAGGGTCCAGCCCT 563
Qy	301	GTCAATCGGGGGAACACTTCAACCTCAAGGCGAGCGGGCAACGACCGCAACCGGATC 360
Db	564	GTCAATCGGGGGAACACTTCAACCTCAAGGCGAGCGGGCAACGACCGCAACCGGATC 623
Qy	361	GTGCTGCTTTTCAAGTTTCGCTCGCGAGGTCTCTATACGTTCGCTGTGGAGGCGTGGAT 420
Db	624	GTGCTGCTTTTCAAGTTTCGCTCGCGAGGTCTCTATACGTTCGCTGTGGAGGCGTGGAT 683
Qy	421	TCCAGTAATGACACCGTTCAACCTGACAGTATTAATTGAAGGCTTCTCACTCGGGCATG 480
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Qy	481	ATCAACCCGAGCGGAGTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db	744	ATCAACCCGAGCGGAGTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
Qy	541	TATCAGATCCGCGTGACCTGTGATGACTACTACTATGGCTTTGGCTGYAATAGTTCTGC 600
Db	804	TATCAGATCCGCGTGACCTGTGATGACTACTACTATGGCTTTGGCTGYAATAGTTCTGC 863
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RESULT 13

LOCUS CQ727152 5897 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 13086 from Patent WO02068579.  
ACCESSION CQ727152  
VERSION CQ727152.1 GI:42292342

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

Patent: WO 02068579-A 13086 06-SEP-2002;

JOURNAL

PE Corporation (NY) (US)

FEATURES

source

1. 5897 Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"



## ORIGIN

Query Match 99.9%; Score 3651; DB 6; Length 5897;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3651; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 181 CCGGAGACCGAGTGCACCGCGAGGTGTGACACATCTTCAAAGTGTGCTCAAG 240
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DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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DEFINITION Sequence 34 from patent US 6703204.
ACCESSION AR482475
VERSION AR482475.1 GI:47244908
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4855)
AUTHORS Mutter, G. L. and Baak, J. P. A.
TITLE Prognostic classification of breast cancer through determination of
nucleic acid sequence expression
JOURNAL Patent: US 6703204-A 34 09-MAR-2004;
The Brigham & Women's Hospital, Inc.; Boston, MA
FEATURES
source Location/Qualifiers
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ORIGIN
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RESULT 15  
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DEFINITION Sequence 34 from Patent WO0210436.  
ACCESSION AX375031  
VERSION AX375031.1 GI:19169863  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE 1  
AUTHORS Baak,J. and Mutter,G.L.  
TITLE Prognostic classification of breast cancer  
JOURNAL Patent: WO 0210436-A, 34, 07-FEB-2002;  
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)

FEATURES  
Location/Qualifiers  
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Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3650; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 121 TCCATGACAGAACGTGAACCGGGAGCTGCAGAACCGGGAACTGCTGCGCGCGCGCGCGCGGAAC 180  
Db 491 TCCATGACAGAACGTGAACCGGGAGCTGCAGAACCGGGAACTGCTGCGCGCGCGCGCGGAAC 550  
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Db 611 GAGTATCAGTCCCGCTGACGCT 670  
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Qy	CTCTGTGAGTGCATCGATTTATTTGAGGCTAAATCCCTGCCAGAACGGTGCCAGTGC	1620
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 4, 2006, 09:31:09 ; Search time 52 Seconds  
(without alignments)  
1974.294 Million cell updates/sec

Title: US-10-650-650-18

Perfect score: 6248

Sequence: 1 MRSPTTRGRSRLPLSLLLAL.....LIAAIAEVRQRRPLKNRTD 1067

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6024.5	96.4	1220	2 A56136	jagged protein pre
2	2339.5	37.4	1408	2 S16148	gene serrate prote
3	1583.5	25.3	2524	2 A35844	Xotch protein - Af
4	1580.5	25.3	2703	1 A24920	notch protein - fr
5	1562	25.0	2471	2 A49128	cell-fate determin
6	1555	24.9	2437	2 S42612	transmembrane prot
7	1549	24.8	2531	2 A46019	notch-1 protein -
8	1538.5	24.6	2531	2 S18188	notch protein homo
9	1532	24.5	2555	2 A40043	notch protein homo
10	1498.5	24.0	2321	2 S78549	notch3 protein - h
11	1495.5	23.9	2531	2 T31070	notch homolog - se
12	1492	23.9	2352	2 T30201	Notch homolog prot
13	1488	23.8	1064	2 A40136	fibropellin Ia - s
14	1481.5	23.7	2318	2 S45306	notch 3 protein -
15	1467.5	23.5	1203	2 A49175	Notch B protein -
16	1363	21.8	1964	2 T09059	notch4 - mouse
17	1348	21.6	728	2 I50719	C-Delta-1 - chicke
18	1342	21.5	833	2 S19087	gene Delta protein
19	1337	21.4	832	2 A31246	neurogenic protein
20	1337	21.4	880	2 S00670	neurogenic repetit
21	1321.5	21.2	722	2 I48324	DELTA-like 1 - mou
22	1261.5	20.2	2139	2 A35672	crumbs protein - f
23	1243	19.9	685	2 JC7570	Delta-4 protein -
24	1238.5	19.8	686	2 JC7569	Delta-4 protein -
25	1212	19.4	861	2 S06434	Notch homolog Motc
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27	872	14.0	1372	2 T25933	hypothetical prote
28	826.5	13.2	1722	2 B89753	protein Flic7.4 [i
29	825.5	13.2	2918	2 A54105	fibrillin-2 precur

30	824	13.2	2907	2 A57278	fibrillin-2 precur
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32	804.5	12.9	1295	2 A32901	glp1 protein precu
33	797.5	12.8	2871	2 A58567	fibrillin I - bovi
34	796.5	12.7	3002	2 A47221	fibrillin 1 precur
35	792.5	12.7	2871	2 A56224	fibrillin-1 precu
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37	780	12.5	1574	2 T13954	MEGF6 protein - ra
38	779	12.5	1620	2 T27283	hypothetical prote
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40	740.5	11.9	4135	2 T42629	tenascin-X - bovin
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42	733	11.7	1523	2 T13953	MEGF5 protein - ra
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44	700	11.2	4006	2 T09070	probable tenascin
45	699.5	11.2	2201	2 A32160	tenascin-C - human

ALIGNMENTS

RESULT 1

A56136

jagged protein precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 21-Jul-2003

C;Accession: A56136

R;Lindseil, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.

Cell 80-909-917-9095

A;Title: Jagged, a mammalian ligand that activates Notch1

A;Reference number: A56136; MUID:95211842; PMID:7697721

A;Accession: A56136

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1220 <LIN>

A;Cross-references: UNIPARC:UPI000017A1B7; GB:138483

F;379-410/Domain: EGF homology <EGF1>

F;492-523/Domain: EGF homology <EGF>

F;634-665/Domain: EGF homology <EGF2>

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Best Local Similarity 95.8%; Pred. No. 0;  
Matches 1026; Conservative 14; Mismatches 24; Indels 7; Gaps 2;

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Db 820 -----MPG-----APDKALQPH-----CRCAPGWTGLFC 876  
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Db 852 C-----MPG-----APDKALQPH-----CRCAPGWTGLFC 876  
Qy 780 AONTNDCSPHPCVNSGTCTVDGDWYRCCECAPGAGPDCRININECQSSPCAFGATCVDEI 839  
Db 877 AEADQCRGQFCHNGGTCESGAGFRVCAGFGSPGDCRINVNECSPPQCGGATCIDGI 936  
Qy 840 NGYRCVCPGHSAGKCEVSGRP-----CITMGSVIPDGAKM-----DDD 879  
Db 937 GGVSCICPPRGGHGLURCBILLSDPKSACQNASNTISPALNRSONWLIDALTGRTEDDEN 996  
Qy 880 CNTCQCLNGRIAGSKVCMGPRPCL-----LKHGHS---ECPSGQSCIPILDQCFVHPCTG 932  
Db 997 CNACVCENGTSRCTLNLCGLPNCYKVDPLSKSSNLGVCKQHEVCVPALSETCLSSFCNV 1056  
Qy 933 VGEGRSSSLQ-----PVTKC-TSDSYQDNCAINITFTFNKEMSPGLTTEHCSEL 983  
Db 1057 RGDRALEPERRVAPPRLPAKSSCWPNQAVNENCARLTLLALLERVKGASVEGLCSLV 1116  
Qy 984 RNL---NILKNVSAEYS-----IYIACEPSPSANNEIHAISAEDIRDDGNPIKEITDKI 1035  
Db 1117 RVLLAAQLIKPASTFQDQFGLMLVLCIDLTGTNDTVELTVSSSKLMDPOLPV--AVGLL 1174  
Qy 1036 IDLVSRKDRGNSSLIAAFAVRVQR 1060  
Db 1175 GELLSSRLNG-----IQRR 1189

RESULT 3  
A35844  
Xotch protein - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 12-Oct-1990 #sequence\_revision 12-Oct-1990 #text\_change 05-Oct-2004  
R:Accession: A35844  
R:Coffman, C.; Harris, W.; Kintner, C.  
A:Title: Xotch, the Xenopus homolog of Drosophila notch.  
A:Reference number: A35844; MUID:90385285; PMID:2402639  
A:Accession: A35844  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-2524 <COF>  
A:Cross-references: UNIPARC:UPI00004F253  
A:Superfamily: notch protein; ankyrin repeat homology; EGF homology  
C:Keywords: transmembrane protein  
F:146-177/Domain: EGF homology <EGX1>  
F:184-215/Domain: EGF homology <EGF1>  
F:222-254/Domain: EGF homology <EGF>  
F:456-487/Domain: EGF homology <EGX2>  
F:757-788/Domain: EGF homology <EGF3>  
F:1025-1056/Domain: EGF homology <EGX3>  
F:1924-1956/Domain: ankyrin repeat homology <AN1>  
F:1957-1989/Domain: ankyrin repeat homology <AN2>  
F:1991-2023/Domain: ankyrin repeat homology <AN3>  
F:2024-2056/Domain: ankyrin repeat homology <AN4>  
F:2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match

25.3%; Score 1583.5; DB 2; Length 2524;

Best Local Similarity 30.7%; Pred. No. 1.9e-83;  
Matches 348; Conservative 126; Mismatches 335; Indels 323; Gaps 40;  
Qy 62 GDRKCTRDECDTYFKVKLKEYQSRVITAG-PC-----SFG 95  
Db 19 GLRPTQTQA-----EMCLNGRCERTPGGTGVCGLNLYFGERCOFPNPTCTIKQCNVFG 73  
Qy 96 SGSTPVIQGNFTNLKASRGNDRNRIIVLPFSFANPRSYTLLVEAWSSNDTVQPDISIIEKA 155  
Db 74 T-CEPVLQGN-----AIDFICHCPVGFT-----DKV-----CLTPV 103  
Qy 156 SHSGMNPSPQWOTLKQNTGVAFHFEYQIRVTCDYDYFGCNKF-----CRP 202  
Db 104 DNACVANNPCRNCGTCELLNSVT--EYKCR--CPGWTGDSQQADPCASNPANGGKCLP 159  
Qy 203 RDPFFGHYACDQNGKNTCMEGWMP-----ECNRAICRQG--CSPKHGSKCLPGDCRC 253  
Db 160 ---FEIQYIC-----KCPGFHGAACKQDINESQNPKNGGQCINEFYSR---CTC 206  
Qy 254 QYQWQGLYCDK---CIPHPGCVHGI CNE-----PMQCLCETNMGWGLCDKDLNYCGTHQP 305  
Db 207 QNRFTGRNCDPEYVPCNPSPCLNGGTCRQTDTSYDCTCLPGFSGQNCENIIDDPSNN- 265  
Qy 306 CLNGGTCSTNTPDKYOCSCPEGYSGPNC--EIAEHACLSDPCHNRGSKETSLSGFCECS 363  
Db 266 CRNGGTCVD--GVNTYNCQCPDWTGYCTEDVDECQMLPNACQNGGTCHNTYGGYNCVCV 324  
Qy 364 PGWTGPTCSNIDDCSPNNCSHGTCQDLVNGFK----- 397  
Db 325 NGWTGEDCSENIIDCANACHSATSATCHDRVASFYCECPHRTGLLCHLDNACISNPNCEG 384  
Qy 398 -----CVCPPQWMTGKTQOLDANECB--AKPCVNAKSKCNLIASYCDCLPGW 442  
Db 385 SNCDTNPVNGKAICTCPGYTGACNNDVDECSLGANPCERGCRTNLTGSCFQCNCQGY 444  
Qy 443 MGQNCININDCLGQ--CONDASCRDLVNGYRCICPGYAGDHCDERDIDECASPLNGGH 501  
Db 445 AGPRCIDVNECLSNPCQNDSTCLDQIGBFCQICMPGYEGLYCETNIDECASNPCLHNGK 504  
Qy 502 QONEINRFQCLCPTGFSNGLQDIDYCEPNPQNGAQCYNRASDYFCCKPEDEYEGNCS 561  
Db 505 CIDKINEFRCDCTGFSNGLCQHDDECTSTPCNKAQKCLDGPNSYTCQCTEGFTGRHCE 564  
Qy 562 HLKDHCRITTPCEVIDSC-----TVAMASND----- 586  
Db 565 QDINECIPDPCH--YGTCKDGIATFTCLCRPGYTGRLCDNDINECLSKPLNGGQCTDREN 623  
Qy 587 -----TPEGVRYI-----SSNVCGPHGKCKSSGGKFTCDCKNGFTGTTCHEINID 632  
Db 624 GYICTCPKGTGVNCEYTKIDDCASNLC--DNKCKIDKIDG--YECTCEPGYTGKLCNININE 681  
Qy 633 CESNPCRNGGT-----CIDGVNSYKIC 655  
Db 682 CDSNPCRNGGTCKDQINGFTCVCPDGYHDMCLSEVNECSNFCIHGACHDGVNGYKDC 741  
Qy 656 SDGMEGAYCETNINDCSQNPCHNGGTCRDLVNDFYCDCKNGWKGTCHSRDSQDEATCN 715  
Db 742 EACWSGSCNCDINNNECESNPNNGGTCXDMTGAVICTCKAGFSGPNQNTNINESSNPCL 801  
Qy 716 NGTCTYD-----EGDAFKCMCPGGW 735  
Db 802 NHGTCIDDVAGYKCNMCLPYTGAICEAVLAPCAGSPCKNGRCKESDPTFCCECPGW 861  
Qy 736 EGTTCNIAIRNSSCLPNPCHNGGTCVNVGSEFTCVCKEGWEGPTCAONTNDCSPHPCVNSG 795  
Db 862 QGQTCBIDWN--ECVNRPCRNGATQNTNGSYKCNKPGYTGRCNCEMDIDDCQNPCHNGG 920  
Qy 796 TCVDGDNWYRCCECAPGAGPDCRININECQSSPCAFGATCVDEINGYRCVCPFGHSGAKC 855  
Db 921 SCSDGINMPFCNCFAGFRGPKCEEDINECSNFCNKGANCTDCVNSYTCCTCQFGFSGIHC 980  
Qy 856 QEVSGRPCTMTGSVIPDGAKWDDDCNTCQCLNRIACSKVWCGPRPCL--LKHGHSCEP- 912

Db 981 E--SNTP-----DCTESSCFNG-----GTCIDGINTFTCCPP 1011

Qy 913 --SQSCIPILDDCFVHPCTGVGECRSSLSLPVKTKTSDSYQD-NCANI 961

Db 1012 GFTGSYQHDH-NECDSPCLNGTGCDSY---GTYKCTCPQGYTLNCCQL 1059

RESULT 4

A24420

notch protein - fruit fly (*Drosophila melanogaster*)

N:Alternate names: neurogenic repetitive locus protein

C:Species: *Drosophila melanogaster*

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 05-Oct-2004

C:Accession: A24420; A24768; S09358; A05267

R:Kidd, S.; Kelley, M.R.; Young, M.W.

Mol. Cell. Biol. 6, 3094-3108, 1986

A:Reference number: A24420; MUID:87064624; PMID:3097517

A:Accession: A24420

A:Molecule type: DNA

A:Residues: 1-2703 <KID>

A:Cross-references: UNIPROT:P07207; UNIPARC:UPI000016BCC6; GB:K03508; NID:g157991; PID:R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.

Cell 43, 567-581, 1985

A:Reference number: A24768; MUID:86079539; PMID:3935325

A:Accession: A24768

A:Molecule type: mRNA

A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, 'R':Tautz, D.

A:Cross-references: UNIPARC:UPI0000173D1F

A:Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044

Nucleic Acids Res. 17, 6463-6471, 1989

A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA markers

A:Reference number: S09358; MUID:89385974; PMID:2780284

A:Accession: S09358

A:Molecule type: DNA

A:Residues: 2505-2553, 'OQQQ', 2552-2576, 'E', 2578-2604 <TAU>

A:Cross-references: UNIPARC:UPI0000173D20

R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.

Cell 40, 55-62, 1985

A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other

A:Reference number: A05267; MUID:85099329; PMID:2981631

A:Accession: A05267

A:Molecule type: DNA

A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>

A:Cross-references: UNIPARC:UPI0000173D21

C:Genetics:

A:Gene: notch; opa

A:Cross-references: FlyBase:FBgn0004647

A:Map position: 8.96-9.36

A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3

C:Superfamily: notch protein; ankyrin repeat homology; EGF homology/3

C:Keywords: differentiation; tandem repeat; transmembrane protein

F:27-43/Domain: transmembrane #status predicted <TMW1>

F:297-328/Domain: EGF homology <EGX1>

F:530-561/Domain: EGF homology <EGF1>

F:568-599/Domain: EGF homology <EGF>

F:988-1019/Domain: EGF homology <EGX2>

F:1064-1095/Domain: EGF homology <EGF3>

F:1187-1218/Domain: EGF homology <EGX3>

F:1746-1762/Domain: transmembrane #status predicted <TMW2>

F:1950-1982/Domain: ankyrin repeat homology <AN1>

F:1983-2015/Domain: ankyrin repeat homology <AN2>

F:1988-2004/Domain: transmembrane #status predicted <TMW3>

F:2017-2049/Domain: ankyrin repeat homology <AN3>

F:2050-2082/Domain: ankyrin repeat homology <AN4>

F:2083-2115/Domain: ankyrin repeat homology <AN5>

F:2538-2568/Region: Glutamine-rich

F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 25.3%; Score 1580.5; DB 1; Length 2703;

Best Local Similarity 28.1%; Pred. No. 3e-83;

Matches 374; Conservative 139; Mismatches 432; Indels 385; Gaps 47;

Db 1219 ELNIDDCAPNCPQNGGTCFDRVMNFSCSPGPTGMIICBINKODCKPGACHNNGSCIDRV 1278  
Qy 859 SGRPCITWGSVIPDGAWDDDCNTC---QCLN-GRIAC---SKVMCGPRPCLLLHKHSE 910  
Db 1279 GGFECVCPQGFV--GARCEGDINECLNSPCSNAGTLDVQVNNYHCNCRP-----GH-- 1329  
Qy 911 CPSSQSCIPILDQCFVHPCTGVGEBCR-----SSSQPVTKTCTSDSYQ 955  
Db 1330 --MGRHCEHKV-DFCAQSPQNGGNCNIRSGHHCICNNGFYGNKNCBSLQDQDCDSNCRV 1386  
Qy 956 DNCANITFTNKEMMSP-GLTTEHCISELNRLNLKNSAEYSIYIACEPSPSANNEIHV 1014  
Db 1387 GNCVVADEGFGYRCPRGTGHEH-----CEIDTLDCESPNCAQ----- 1426  
Qy 1015 AISAEIDRDD 1024  
Db 1427 GAACEDLLGD 1436  
RESULT 5  
A49128  
cell-fate determining gene Notch2 protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Oct-2004  
C:Accession: A49128  
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.  
Development 116, 931-941, 1992  
A>Title: Notch2: a second mammalian Notch gene.  
A:Reference number: A49128; MUID:93202015; PMID:1295745  
A:Accession: A49128  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-2471 <WE1>  
A:Cross-references: UNIPROT:Q9QW30; UNIPARC:UPI000004F255  
A:Experimental source: Schwann cell  
A>Note: Sequence extracted from NCBI backbone (NCBIP:127811)  
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F:264-295/Domain: EGF homology <EGX1>  
F:799-830/Domain: EGF homology <EGF1>  
F:877-908/Domain: EGF homology <EGX2>  
F:1029-1060/Domain: EGF homology <EGF>  
F:1067-1098/Domain: EGF homology <EGX3>  
F:1153-1184/Domain: EGF homology <EGF3>  
F:1191-1222/Domain: EGF homology <EGX4>  
F:1876-1908/Domain: ankyrin repeat homology <AN1>  
F:1909-1941/Domain: ankyrin repeat homology <AN2>  
F:1943-1975/Domain: ankyrin repeat homology <AN3>  
F:1976-2008/Domain: ankyrin repeat homology <AN4>  
F:2009-2041/Domain: ankyrin repeat homology <AN5>  
Query Match 25.08; Score 1562; DB 2; Length 2471;  
Best Local Similarity 29.68; Pred. No. 3.3e-82;  
Matches 326; Conservative 122; Mismatches 326; Indels 328; Gaps 34;  
Qy 186 TCDDYVYFGCNKFRPRDDFFGHYA-----CDQN-----GNKT--CWEGW 224  
Db 40 TCVTYHNGTG---YCRCEPGLGEYCOHRDPCEKNRCQNGGTCVTQAMLKATCRCAPGF 96  
Qy 225 MGPECNRAI-----CRQGSPPHGSCKLPG-----DCRCQVWQGLYC-----DKCIPH 268  
Db 97 TGEDCQVSTSHPCFVSFRPCQNG-----GTCHLSWDTYECTCQVGFQKOCOWTDVCLSH 151  
Qy 269 PGCVHVG-----ICNEPWOCLCETNWWGQCLDKLNYGTHQPCNLNGTCSNTGPDKYQCS 323  
Db 152 P-CENGSTCSVANQ--FSCRCAPAGITQKCDADINECDIFGRCHQGGTCLNL--PGSTRQ 208  
Qy 324 CPFGYSGNCEIAEHAACLSDFCHNRGSKET--SLGFCEGSPGWGTCTSTNIDDCSPNN 382  
Db 209 CPQRFTHQCHDSPPVPCAPSPCVNGGTCRGTGDTSECHCLPGFEGSNCRNIDDCPNHK 268  
Qy 383 CSHGHTCQDLVNGFKVCCPPQWTGKTCQLDANEC----- 416

Db 269 CQNGGVCVGVNTYNCRCPPQWTGQFCTEDVDBCLLIQPNACQNGGTCNRRNGGVCVCVN 328  
Qy 417 ----- 416  
Db 329 GWSGDDCSENIIDCAFASCTPGSTCIDRVASFCLCPGEGKAGLLCHLDDACISNPKHGA 388  
Qy 417 -----BAKPCVNAKSKRLIASYVYCDCLPGW 442  
Db 389 LCDTNPLNGQYICTCPQAYKAGDCTEDVDECAMANSNPECHAGKCVNTDGAFCHECLKG 448  
Qy 443 MGQNCQDININDLQGO--CONDASCRDLVNGYRCICPGYAGDHCERDIDECASNPCLNGGH 501  
Db 449 AGPRCEMDINECHSDFCQNDATCLDKIGFTCLCMFGFKGVHCELVNEVQSPCVNNGQ 508  
Qy 502 CQNEINRFQCLCTPGFSGNLQCLDIDYCEBNPCQGAQCYNRASDYFCCKPEDEYEGNCS 561  
Db 509 CVDKVNRFQCLCPPGFTGPVCQIDIDDSCSTPLNGAKCIDHPNGYECQCATGFTGLCD 568  
Qy 562 HLKDHCRTPC-----EVIDSCTVAMASND----- 586  
Db 569 ENIDNCDPDPCHRGQCGQDGIDSYTCICNPGYMGALCSQDIDECYSFPLNDGRCLDLVNG 628  
Qy 587 -----TPGVRV-----ISSNVCGPHGKCKSQSGKFTCDCKNGFTCTYCHENINDC 633  
Db 629 YQCNQCPGTSLGNCBINFDDCASNPC--LHGAC--VDGINRYSCVCSPGFTQRCNIDDEC 686  
Qy 634 ESNPCRNNGTCTIDGVN-----SYKICIS 656  
Db 687 ASNPCKDATCINDVNGFRCMCPGPHHPSCYSQVNECLSSPCIHGNGTGLSGYKCLCD 746  
Qy 657 DWEGAYCETNINDCSQNPCHNGGTCRDLVNDYCDCKNGWKTKTCHSRDSQDDEATCNN 716  
Db 747 AGWVGINCEVDKNECLSNPCQNGGTCNNLVNGYRCTCKGFKGYNCQVNIDECASNPCLN 806  
Qy 717 GCTCYDEGDAFKCMCPGEGTTCNTARNSSCLPNCHNGGTC--VVGESFTCVCKEGW 774  
Db 807 QGFCLDDVSGYTCHMLPYTGKNCQTVL--APCSNPNCENAAVCKEAPNFSFTCLCAPGW 865  
Qy 775 EGPICAQNTNDCSPPHPCYNSTGTCVDGDNWYRCAPGAGPDCRININECQSSPFCAGAT 834  
Db 866 QGQRCITVDVDECVSKFCMNGICHNTQSGYMCCECPGFGSGMDCDEEDNCLANPCQNGS 925  
Qy 835 CVDEINGYRCVCPGHSAGKQ---EVSGRPCITWGS-----VLPDG-----A 874  
Db 926 CVDKVNFTFCLCLPGFVGDKCQTDNNECLSEPCKNGGTCSDYVNSYTCCTCPAGFHGVHCE 985  
Qy 875 KWDDDCNTCQCLNG-----RIACSKVMCGP-----RPCL-----LH 905  
Db 986 NNIDECTESSCFNGGTCVDGINSFSCLCVPVGTGPFCLHDINECSNPCLNSGTCTVDGLG 1045  
Qy 906 KGHSECP---SGQSCIPILDQCFVHPCTGVGECRSSSLQPVTKTCTS-----DSYQDNC 958  
Db 1046 TYRCTCLPGYTGKNC--QTLVNLCSPPCKNKGTCQAQEKARP---RCLCPPGWDGAY---C 1098  
Qy 959 ANITFTFNKEMMSPGLTTEHIC 980  
Db 1099 DVLNVSCAAALQKGVPEVHLC 1120  
RESULT 6  
S42612  
transmembrane protein precursor - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S42612  
R:Bierkamp, C.; Campos-Ortega, J.A.  
Mech. Dev. 43, 87-100, 1993  
A>Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern o  
A:Reference number: S42612; MUID:94128602; PMID:8297791  
A:Accession: S42612  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-2437 <BIE>

A;Cross-references: UNIPROT:P46530; UNIPARC:UPI000013056E; EMBL:X69088; NID:9433866; PID:1027		Db		862 QTC-EVDINECVRNPNCTNGVGCENLFR-----GGFQCRC-----NPGF 897	
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology		Qy		975 TTEHCSELRLNLIKLVSAEYSIYIACRPPSANNEL-----HVAISAEIRDGNNP 1027	
F;755-786/Domain: EGF homology <EGF1>		Db		898 TGA-LCE-----NDIDD-----CEPNPCSGVGCQDRVNGFVCVCLAGFR--GER 939	
F;1023-1054/Domain: EGF homology <EGF2>		Qy		1028 IKEITDKIIDLVSKRDGN 1045	
F;1185-1216/Domain: EGF homology <EGF2>		Db		940 CAEDIDECVSAPCRNGGN 957	
F;1915-1947/Domain: ankyrin repeat homology <AN1>		RESULT 7			
F;1948-1980/Domain: ankyrin repeat homology <AN2>		A46019			
F;1982-2014/Domain: ankyrin repeat homology <AN3>		N;Alternate names: notch protein			
F;2015-2047/Domain: ankyrin repeat homology <AN4>		C;Species: Mus musculus (house mouse)			
F;2048-2080/Domain: ankyrin repeat homology <AN5>		C;Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 05-Oct-2004			
		C;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S2109			
		R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid-			
		Genomics 15, 259-264, 1993			
		A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of			
		A;Reference number: A46019; MUID:93194170; PMID:8449489			
		A;Accession: A46019			
		A;Status: not compared with conceptual translation			
		A;Molecule type: nucleic acid			
		A;Residues: 1-2531 <DEL>			
		A;Cross-references: UNIPARC:UPI0000177461; EMBL:X68278; NID:g281			
		A;Experimental source: embryo			
		A;Note: sequence extracted from NCBI backbone (NCBIP:127318)			
		R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; I			
		submitted to the EMBL Data Library, April 1992			
		A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest			
		A;Reference number: S25144			
		A;Accession: S25144			
		A;Status: preliminary; nucleic acid sequence not shown			
		A;Molecule type: mRNA			
		A;Residues: 1161-1547 <LAR>			
		A;Cross-references: UNIPARC:UPI0000177462; EMBL:X68278; NID:g287987; PID:CAA48339.1; PI			
		A;Experimental source: embryo			
		A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)			
		C;Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.			
		C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe			
		C;Genetics:			
		A;Gene: notch-1			
		A;Map position: 2			
		A;Note: proximal region of chromosome 2			
		C;Superfamily: notch protein; ankyrin repeat homology; EGF homology			
		F;106-138/Domain: EGF homology <EGF1>			
		F;144-175/Domain: EGF homology <EG01>			
		F;222-254/Domain: EGF homology <EGF2>			
		F;261-292/Domain: EGF homology <EG02>			
		F;339-370/Domain: EGF homology <EG03>			
		F;416-449/Domain: EGF homology <EGF3>			
		F;456-487/Domain: EGF homology <EG04>			
		F;494-525/Domain: EGF homology <EG05>			

Query Match 24.9%; Score 1555; DB 2; Length 2437;		Query Match 24.9%; Score 1555; DB 2; Length 2437;	
Best Local Similarity 32.8%; Pred. No. 8.1e-82;		Best Local Similarity 32.8%; Pred. No. 8.1e-82;	
Matches 321; Conservative 115; Mismatches 317; Indels 225; Gaps 34;		Matches 321; Conservative 115; Mismatches 317; Indels 225; Gaps 34;	
Qy		200 CRPRDDFFGHYACDQNGKT-----CMEGW-----MGPECNRAICROGCSFKHGSK 246	
Db		73 CRPQ-----MQNEVGKDCVLFGRDLRLCTPVNHACMNSPCRG-----GTCS 117	
Qy		247 L-----PGDCRCOVGMGLYC---DKCIPHPGCVHIGCN---EPWOCLCETNMGQLCDKD 296	
Db		118 LTLDTTCRCQPGWSKTLQALDPCASNPANGGQCSAFESHYICTCPNFHGTQCRQD 177	
Qy		297 LNYCG--THQCLNGGTCSTGPKYQCSCEPGYSGPNCETAEHACLSDPCCHNRGSKETS 355	
Db		178 VNECAVSPSCRNGGTCTINE--VGSYLRCRPPETGPHCQRLYQCLPSPCRSGGTCTQTS 236	
Qy		356 -LGPECCSGPGWGTCTSTNIDDCSPNNSHGTCQDLVNGFKVCVPQWTGKTCQLDAN 414	
Db		237 DTHTCSCLPFGTQTCHEHNVDCTQHACBNGGPGCIDGINTYCHDKHWTGQVCTBEDVD 296	
Qy		415 ECEAKP--CVNAKSKNLASYCDCLPGMWGQNCININDCL--GOCONDASCRDLVNGY 471	
Db		297 ECELSPNACNGGTGCHNTIGGFHCVCVNGWGTDDCSENIDDCAASASHGATCHDRVASF 356	
Qy		472 -----RCICPPGYAGDHCDERIDDECA 492	
Db		357 FCBCPHGRTGLLCHLDACISNPKQSGNCDTNVPSKCAICTCPPGYGSACNQDIDEC 416	
Qy		493 --SNPLNGHGCNEINRFLCPTGFSGNLCQLDIDYCEPNPCQGAOCYNRASDYFCK 550	
Db		417 LGANPCEHGRCLNTKGSFQCKLQYEGRCPEMDVNECKSNPCQNDATCLDQIGGFHCI 476	
Qy		551 CPEDYEGKNSHLKHCRTPCEVIDSCYVAMASNDTPGVRYISSNVCPGPHGCKQSOG 610	
Db		477 CMPGYEGVFCQNSDDCASQPC-----LNGKCIDKI- 507	
Qy		611 GKFTCDCKNGFTGYCHENINDCESNPRNGGTCIDGVNSYKTCSDGWEGAYCETNND 670	
Db		508 NSFHCECPKFGSGLCQVDVDECASTPCKNCAKTGDPNKYTCBCTPFGSGIHCELDINE 567	
Qy		671 CSQNPCHNGTCRDLVNDIFYCDKNKWKGTCHSRDSQCDBATCNGGTCYDEGDAPKCM 730	
Db		568 CASSPCHY--GVCRDGVASFCTCDRPGYTGRILCETNINECLSQPCRNNGTQCDRENAVICT 626	
Qy		731 CP-----GGWECTNCIARNSSCLNPPC 753	
Db		627 CPKGTGTGNCBINTDDCKRKPCDYGKIDKINGVEYCEPQYSGSMCNII--NIDCALNPPC 685	
Qy		754 HNGGTCVVGSGSFTCVCKEGWEGICAQNTWDCSPHPCYNSGTCVDGDNWYRCBCAPGFA 813	
Db		686 HNGGTCIDGVNSFTCLCPDGRDATTCLSQHNECSSNPCIH--GSLCDQINSYRCVCEAGWM 744	
Qy		814 GPDGRININECQSPFCATGATCVDEINGYRCVPPHSGAKCQ-----EVSGRPCITMGVS 869	
Db		745 GRNCDININECLSNPCVNGGTCCKMTSGYLCTCRAGFSGPNPCOMNINECASNPCLNQSG 804	
Qy		870 IPDGAKWDDCNTCOCLNGRTACSKVM--CCPRPCL-----LHKHSECPSS---G 914	
Db		805 IDDVAGF--KCNCLMPLPYTGEV--CENVLAPCSFRPCKNGGVCRESEDFQSFSCNCPAQWQ 861	
Qy		915 QSCPIPLDDQCFVHPCTGVGECRSSLSLPVTKTCTSDSYQDNCANITFTFNKEMMSFGL 974	

Qy	718	GTCYDEGDAFKCMCPGGWEGTTCNIARNS	-----SCLNPNCHNGTCTVVGNSFTCVCKEKGWGPICANTNDSCSHPH	790
Db	1072	GRCWQNTQYHCECRSGMTGNCVLSVCEVAQKRGIDVTLCCQHGGLCVDEGDKHYC	1133	
Qy	747	-----SCLNPNCHNGTCTVVGNSFTCVCKEKGWGPICANTNDSCSHPH	790	
Db	1132	HQAGYATGSGYCEDVEDECSNPQNGATCTDYLGGFSCKVAGYHGSNCSEINECLSQP	1199	
Qy	791	CYNSGTCTVDGDNWYRCACPGFAGPDCRINIEC	-----QSSPCAFGATCVDDEINGY	842
Db	1192	CQNGTCTDILTNSYKCSCPRTQVHCIEINDDCHPPLDPASRSPKCFNNGTCTVDQVGGY	1251	
Qy	843	RCVCP	-----GHSAGKACQEV	858
Db	1252	TCTCPFGVGERCBGDVNECLSNPDRGTQNCVQRVNDHFCECRAGHTGRRCESVINGC	1311	
Qy	859	SGRPCITWGSVIP	-----DGAKWDDDCNTC	899
Db	1312	RGKPCKNNGYCAVASNTARGFICRPAGFEGATCENDARTCGSLURCLNGGTCTCIS	-----GP	1367
Qy	900	RP	-----PSQSCIPILDDQCFVHPCTGVGECRSSLSLP	943
Db	1368	RSPTCLCLGSGFTGPECFPASSPCVG	-----SNPCYNQGTCTPTSEN	1410
RESULT 8				
S18188				
notch protein homolog - rat				
C:Species: Rattus norvegicus (Norway rat)				
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002				
C:Accession: S18188				
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.				
Development 113, 199-205, 1991				
A>Title: A homolog of Drosophila Notch expressed during mammalian development.				
A:Reference number: S18188; MUID:92111383; PMID:1764995				
A:Accession: S18188				
A:Molecule type: mRNA				
A:Residues: 1-2531 <WEI>				
A:Cross-references: UNIPARC:UPT000177456; EMBL:X57405; NID:957634; PID:957635				
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology				
F:987-1018/Domain: EGF homology <EGF>				
F:1025-1056/Domain: EGF homology <EGF>				
F:1233-1264/Domain: EGF homology <EGF2>				
F:1917-1949/Domain: ankyrin repeat homology <AN1>				
F:1950-1982/Domain: ankyrin repeat homology <AN2>				
F:1984-2016/Domain: ankyrin repeat homology <AN3>				
F:2017-2049/Domain: ankyrin repeat homology <AN4>				
F:2050-2082/Domain: ankyrin repeat homology <AN5>				
Query Match 24.6%; Score 1538.5; DB 2; Length 2531;				
Best Local Similarity 31.7%; Pred. No. 7.5e-81;				
Matches 305; Conservative 120; Mismatches 316; Indels 221; Gaps 26;				
Qy	186	TCDYVYGF	-----NKFRCPRDDFFGHYACDQNGNKT	229
Db	466	TCLDQIGEFQICMPGYEGVYCEINTDECASSPLCHNGRCVDKINEFLCQCPKGFSGHL	525	
Qy	230	NRAICRQGS	-----DCRCQYHQGLYC	278
Db	526	QYVDECASTPCNKGAKCLDGPNTYTCVCTEGYTGTHCEVDI	584	
Qy	279	PMOCLCETNWGQ	-----DNCYCTHPCPLNGGTCTSGTDPKYOCSPGEGVGNPCIRAE	337
Db	585	ATFTCLCQPGYTHHCHETNINECHS	-----OPCHHGGTCQDR	642
Qy	338	HACLSDPCHNRGCKETS	-----SLGFECECSPGWGTPTCTSTNIDDCSPNNCSHGCTCDLVNFGFK	397
Db	643	DDCASNPC	-----DSGTCLDKIDGVEACACEPGYTGSMCNVNIDECAGSPCHNGTCTCEDGIAGFT	701
Qy	398	CVCPPQWTKTCLDANECAKFCVNAKS	-----CKNLIASVYCDCLPGWGMQNCIDINIDC	456
Db	702	CRCEGYHDP	-----PTCLSEVNECNSNCFI	760







Db 1073 PEGRGSHCHQEVDPCLAPQCHGCTCR-GYMGYMCECL-PGVNGDNCEDDVDECASQP 1130  
Qy 970 MSPG-----LTTTHHCS-EURNLNILKNVSAEYSIYIACEPSP 1006  
Db 1131 CQHGSGCIDLVARYLCSPPGTGLVLCINEED-----DCQPGP 1168  
RESULT 11  
T31070  
notch homolog - sea urchin (Lytechinus variegatus)  
C;Species: Lytechinus variegatus (variegated urchin)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
C;Accession: T31070  
R;Sherwood, D.R.; McClay, D.R.  
Development 124, 3363-3374, 1997  
A;Title: Identification and localization of a sea urchin Notch homologue: insights into  
A;Reference number: Z20966; MUID:97454256; PMID:9310331  
A;Accession: T31070  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2531 <SHE>  
A;Cross-references: UNIPARC:UPI000007E31C; EMBL:AF000634; NID:g2570350; PID:g2570351; PI  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
Query Match 23.9%; Score 1495.5; DB 2; Length 2531;  
Best Local Similarity 27.8%; Pred. No. 2.2e-78; Indels 357; Gaps 36;  
Matches 334; Conservative 136; Mismatches 376;  
Qy 51 NGNCC-----GGARNPGDRKTRDECDTYFFVKVLKEYOSRYTAGGPCSFGSGSTPVIGNT 106  
Db 213 NGGTCFNQYGGFCCEPLGFTGQCELVYRPSD-----PCRNG-GQCASTGPT 262  
Qy 107 FNLKASGNDRNIVLPFSFANPRSYLLVEAMDSSNDTVQPSIIEKASHGMINPSRQ 166  
Db 263 FTCTCQNGFTGETCEL-----NLNDCTQHQLNGGTCIDGVNDYT-- 302  
Qy 167 WQTLKQNTGV-AHPEY-QIRVTCDDYYGFGKNKFCRPRDDFFGHVACDQNGKNTCMEGW 224  
Db 303 CSCLEFTGYVCEMDFDECDAVDPCFNGGTCS-----NTYGNFSC-----ICVRGW 349  
Qy 225 MGPECNRAICRQGSPPKHGSKLPGDCR-----COYGWQGLYC---DKCIPHPGV 272  
Db 350 EGQTCF--INKDDCTP--NPFQFGECEDRVASPKCTCPGRTGLLCHLEDAQMSNP-CH 404  
Qy 273 H-----GTCNE-----PWQCLCE 285  
Db 405 HTAQCTSVVDGSPICDCAATGYQGFNGSEDIDECLSMDSICQSGGTCCQNFPGGWSCLCS 464  
Qy 286 TNNWGQLCDLNYCGTHQPLCLNGTCSNTGPDKYQCSCEPGYSGPNCEIAEHAELSDPC 345  
Db 465 SGFTGSRCETDIDEC-DDDPCYNGGTCLNK-RGGYACILTGFTGTLCETDINECSSNPC 522  
Qy 346 HNRGSKETSILGFCEGSPGWTGPTCTNTIDDCSPNNCSHGTCQDLVNGFKVCYCPQWT 405  
Db 523 LNGASCDFITGRFECACLAGYTGTTCCQVNIIDDCQSPCENGGTCTDGVNQFTCLCETGYE 582  
Qy 406 GKTQLDANECEAKPCVNAKSKNLIASYYCDCLPGMWQNCNDINIDCLGQ-CONDASC 464  
Db 583 GHRCEMDSDECAFRPMNGGVCEDLIGFYQCNCPVGTSGDNCENYHDCSSNPNVNDGTC 642  
Qy 465 RDLVNGYRCICPPGVAGDHCHERDIDECASNPLNGHCHONEINFCQLCPTGFSGNLCQL 524  
Db 643 VDGINEYTCMEHGRGLNCEEDIDDCSRPCHNGGTCTVDVNGYHCLCPYGHDPFMS 702  
Qy 525 DIDYCEPNPONGAQCYNRASDYFCKPEDYEGKNCESHLKDHCRTPCE----- 573  
Db 703 NINECSSNPNVNGSGCHDVNGVEYCECMAGYTGTRCTDDDFDECSSNPNQCHGGTCDNRHAF 762  
Qy 574 -----VIDSCVTAMSN-----DTPGVRVY-----S 595  
Db 763 YNCTCOAGYTGNGCEVNIIDDCVDFCLNGGTCTIDEVNSFCQCPQTFFVLLCETERSPCE 822  
Qy 596 SNVCGPHGKC-KSQSGGKFTCDCKNGFTGTGTCHENINDCESNPNCRNGGTCTIDGVNSYKCI 654

Db 823 DNOQNGATCVYSEDYAGYSCRTSGFQGNFCDDDRNECLFSPCRNGSGCTNLEGSFCS 882  
Qy 655 CSDGWEGACVETNINDCONPNCHNGTCDRLVNDFYCDCKNGHKGKTKCHSRDQCEATC 714  
Db 883 CLPGYDGPICEINIDRECAAGPCTNGGICTDLIDDYFCSCQGRFTGKNCQNDTDECLSSPC 942  
Qy 715 NNGGTCYDSGDAPKCMCPGSGWEGTTCNI-----ARNSSCL----- 749  
Db 943 RRGATCHEYVDYSYTCCLVFGSMHCEINDQDCTTSCLYGGTCIDGVNSYTCVGTGYT 1002  
Qy 750 -----PNPCHNGG 757  
Db 1003 GSNQIETINECDSPCENGATCQDRFGSYSCHDVGFTGLNCEHVYVQWCSPPNNPCVNGA 1062  
Qy 758 TCVVNG-----ESFTCV 769  
Db 1063 TCVAMGHLYECHCASNWIKGLCDVPKVSCTDIASDRKNVTRSELCLNGGTCTIDATSSHCL 1122  
Qy 770 CKEGWEGPICAQNTNDCSPHPCVNSGTCVDGDNWYRCECAPGFAGPDCRININECOSSPC 829  
Db 1123 CQDGYTGSYCEVNIDECASAPCHNGGTCTDGVSYTCSCLPFGFEGPRCQONINECASSPC 1182  
Qy 830 AFGATCVDEINGYRCVCPGPGHSGAKQEVSGRPCIITMGSVIPDGAKWDDDCNTCQCLNGR 889  
Db 1183 HNGGQCHDMVNGYTCSPAGTQGTDCS-----INL-----DDCYEGACYHGG 1224  
Qy 890 IACSKVWCGPRPCLLHKHSECPGSGQSCPIILDQCFV-HPCTG-VGECHSSSLQPVKTK 947  
Db 1225 VCIDQV--GTYT-----DCPLG-----FVGQHCEDGVNECLSNPCDPVGSQ 1264  
Qy 948 CTSDSYVQDNCAITFTFNKEMMSPLTTEHICSELNMLNKNVSAEYSIYIACEPSPS 1007  
Db 1265 -----DCVQLINNY-QCVCKPGYTGQDCQEIPN-----CQNDPC 1298  
Qy 1008 ANN 1010  
Db 1299 QNN 1301  
RESULT 12  
T30201  
Notch homolog protein - sea squirt (Halocynthia roretzi)  
C;Species: Halocynthia roretzi  
C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 08-Sep-2002  
C;Accession: T30201  
R;Hori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.  
Dev. Genes Evol. 207, 371-380, 1997  
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the cer  
A;Reference number: Z20775  
A;Accession: T30201  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2352 <HOR>  
A;Cross-references: UNIPARC:UPI0000081BFC; EMBL:AB001327; NID:d1204472; PID:d1026501; PI  
C;Genetics:  
A;Gene: Notch  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
Query Match 23.9%; Score 1492; DB 2; Length 2352;  
Best Local Similarity 28.7%; Pred. No. 3.3e-78;  
Matches 370; Conservative 126; Mismatches 409; Indels 382; Gaps 45;  
Qy 49 LONGNCCGGARNPGD--RKCTRDECDTYF--KVCLEKYQSRVTAGGPGCSFGSGSTPVIGG 104  
Db 77 LNSGTCAVTELTAQDFSYQCT---CQTGTGDTCT---SQVLVYCSNPNCSNAGACEEL--S 128  
Qy 105 NTFNLKASRG-----NDRNRIPL-----FSPAWRPSYTLVVEAMDSS 142  
Db 129 NSFKCTCTSGYGTCDANDVNECDTPTDICONAGTCSNNDGGYSCS-----CVAGEGN 181  
Qy 143 NDTVQPSIIEKASHSG-----MINPSQWQTLK 171

Dd		182	NCEVNIIDDCSHSCQNGATCADAYSTYDCHCPAEBWTGYCTIIVDECELSNNVKARRDLQ	241
Qy		172	QNTG-----VAHFYQIRVTCDYYGYFGCNKFCRP----	202
Dd		242	QTEGGFTCNVYGFRDDCSNIDDCSNVACFH--NARCIDIAGTPEC--LCTPGNRIL	296
Qy		203	--RDD-----PFHGVACDONGKTCMEGHMGBECNRAI--CRQGSCP-	240
Dd		297	CHLDDACISPCARGATCDTNPIITGHMMCD-----CPDGWTDKDCSKIDIECSLGGNPC	350
Qy		241	-KHGSCKLPG--DCRCOYGMWGLYCD---KCIPHP-----GCVHGICNEBPWOCLCETN	287
Dd		351	EHNQCQNNTDGSFBCICVAGYSGRPCETINIECEPNPCRN DATCLDMIGN--FNVCWMPG	408
Qy		288	WGGQLCDKLNYCGTHOPCLNGGTCSNTPDKYQCSPGEGSYGNCEIAEHACLSDPCNH	347
Dd		409	FTGIICDEDIECESN-PCANGGTICDE-VNAYITCSALGFTGDDCSQIDECASTPCWN	466
Qy		348	RGSCKETSLPFBECBSFGWTGPTGSTNIDD CSPNNCSHHGTCQDLVNGFKVCVPQWTGK	407
Dd		467	KATCIDXANAYECECAPGYTVHCETNIDD CVINPC-HYSGSCRDVNTFYCDLLGYEGT	525
Qy		408	TCOLDANECAKPCVNAKSKNLLASYCDCLPCMGMONCDININDCLGQQNDASCRDL	467
Dd		526	KCOQDTNECASSPCENGCTDEIGYTYCTCPTGTSGSSCEINPDCCVGNPCQYGTCDVG	585
Qy		468	VNGYRICIPCYPAGDHGERDIDECASNPLNGGHGCQNEINRFQCLCP-----	514
Dd		586	VDDYSCSTFGYTGEHCDDTDINECDNSNPCMNGATCQEVNVFVQCQPPGIMGTOCSSDIQ	645
Qy		515	-----	514
Dd		646	ECSSNPCLHEYARRDOHVHCICDAGYOGENCETEINECASNPCQHGAENKVAQFVS HCD	705
Qy		515	TGFSGNLCOLDIDYCEFPNCPONGAQCYNRASDYECKPEDYEGKNC SHLKDXHCFTTICEV	574
Dd		706	AGYTGTA CEIDINECATOPCONGTCTSGINSYNACPAKYTVGNCSTELSPCVNPNPCEN	765
Qy		575	IDSCITVAMASND-----TPGVRVYISSNVCGP-----HGKCKLOS G-----GK	612
Dd		766	GATC--QESADYLAVYCQPEGPR-----GPTCATDINECVNSPCKNGGGCTNLVPG	815
Qy		613	FTDCNKGPFTGYCHENINCESNPCRNGGTCIDGVNSYKCI CSDGWEGAYCFETNIDCS	672
Dd		816	YQCTCSQGF GKDCD TDIDDCSSNPCLNGGQCLDDVGSYKCLCLPFGPEGNNCQBEVNECA	875
Qy		673	QNPCHNGGTCRDLYNDPYCDCKGNWKGTCHSRDSQCD EATCMNGT C-----	720
Dd		876	SFPCKNGGICTDYVNSVYCTCLSGFYSLDCEKNIEDCSSSMNGGTCVDGINSYS CSC T	935
Qy		721	-----YDEGDAFKMCPGGEWGTCTCNIA RNSSCLN P C-----	753
Dd		936	ANFTGDKQNAVNNCASLOQNGGT CYDSDGP-KCA CVHYGTGTHCBESIQNLCTGN I C	994
Qy		754	HNGGT CVVNGESFTCVCKEGWEGPICQNTNDCS-----PHPCYNSGTCDVGDGNW	803
Dd		995	KNGSSCVQTSNTVSCNCLGGVEGTTDCAVPQVSC TVGASLLGIAVSDLCLNGGTCHDSTA	1054
Qy		804	YRECAPGPAPDCRININECQSSPCA FGATCVD EINGYRCVCPPHSGHAKC-----QEVS	859
Dd		1055	HEGSCVAGFTG SYCDIIDIECASVPCKNGATCNDLIN SYSICICALGYEGATCLTD KDECA	1114
Qy		860	GRPCITMGSVI-----PDCAKW-----DDCNTCQCLNGRTACSKVMGGRPCL	903
Dd		1115	SSPCKNGGTCIDRINSFYCSGLAGTBGVLEINEDEBCEINCLNGGVCIDGI--GGFSQC	1172
Qy		904	LHKGH-----SEC-----PSQSQCI-----PILDQQCFVH	928
Dd		1173	CPSGYERRCQGDVNECLSNPCSSPGSLACIQSNSYQCVCADYTGSECOIRIGSCD IN	1232
Qy		929	PCTGVGEC--RSSSLQP VKTKTSDSYQDN CANITTFNKEMMSPLGTTEH-----	978
Dd		1233	FLCNDGICTDNSODIITYKQCOQTW-GYHGKKCE N-----SYSMCSANFFCVCHEAPCODGT	1286

F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-274,451-466,468-477,484-495/Diulfide bonds: #status predicted	
F;489-504,506-515,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-624,626-637,639-650,652-663,665-676,678-689,691-702,704-715,717-728,730-741,743-754,756-767,769-780,782-793,795-806,808-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Diulfide bonds: #status predicted	
Query Match 23.8%; Score 1486; DB 2; Length 1064;	
Best Local Similarity 33.2%; Pred. No. 2.9e-78;	
Matches 326; Conservative 122; Mismatches 393; Indels 140; Gaps 34;	
QY 62 GDRKTRDECD-----TYFKVCLKEYQSRVATAGGPCSFGSGSTPVIIGNTNLKA 111	
DB 19 GQECSDSPCEGSTCQEGSGSYTCQCPMGYD-----GQNCDFRTGSN--CGYNVFDANG 71	
QY 112 -----SRGNDRNRLVLPFSFAWPSYTLLEAVM--DSSNDTVQ-----PDSIIIEKA-- 155	
DB 72 MIDSPNYPAMYNRADCLYLIRTKARSITFTIEDFTVEFKDVVEYIGIPEADFQALG 131	
QY 156 SHSG-----MINPSROWTLKQNTGVAHFEYQIRVTCDDYVYFGNC-KPCR- 201	
DB 132 SFEGNLTQDDVVPAPFTVQDQAWFIFSTDRNIVNRGFRITFSSD-----GDDCDPNLCQN 187	
QY 202 --PRDDFFGHYACQDNKTKMBEGWMGPECNRAI-----CRQGSPPKHGSKLPG--- 249	
DB 188 GAACTDLVNDYAC-----TCCPGFTGRNCBIDIDECASDPQNG-----GAC-VDGVNG 235	
QY 250 -DRCQYQWQGLYCD----KCIHPGCVHIGCNE---PWQCLCETNWGGQLCDKDLNYCG 301	
DB 236 YVCNVCVGFPGDCEENNINECASPLCLNGGICVDGVNMFECTCLAGFTGVRCEVNIDECA 295	
QY 302 THOPLNGGTCSTNTPDKYQCSCEPGYSGNPECIAEHAACLSDPCHNRGSKETSGLGECE 361	
DB 296 S-APCQNGGICID-GINGYTCSCPLGFGSGNCENNDDCCSIFCLNGGTCVDLVNAYMCV 353	
QY 362 CSPGWTGPTCTNIDDCSPNNCSHGTCQDLVNGFKVCVPPQWTKTCTOLDANECEAKPC 421	
DB 354 CAPGWTGPTCADNIDECASAPCQNGGVCIDGVNGYMCDCQPGYGTGTCETDIDECARPPC 413	
QY 422 VNAKSKNLIASYCYDCLPGHMGONCDININDCLGQ--CONDASCRDLVNGYRCLCPGYA 480	
DB 414 QNGGDCVDGVNGVYVCICAPGDFGLNGENNIDECASRPCQNGAVCDGVNGFVCTCSAGYT 473	
QY 481 GDHCERDIDECASNPCLNGHGHCQNEINRFQCLCPTGFGSGLNCQLDIDYCEPNPQNGAQOC 540	
DB 474 GVLCEIDIINECASNPCLNGGVCTDLVNGYICTCAAGFEGTNCETDIDECASFPQNGATC 533	
QY 541 YNRASDYFCCKPEDEYEGKNCSHLKHCRTPTEVIDSCT-----VAMASNDTPGVRYYI 594	
DB 534 TDQVNGYVCTCVPGYTGVLCETDINECASFPCLNGGTCNDQVNGYVCVCAQDTSVSTCET 593	
QY 595 SSNVCGP-----HGKCKSQSGKFTCDKNGKTCIDVNDYFCDCKNGMKGTCHSRDSQC 649	
DB 594 DRDECASAPCLNGGACMDVNGV-FVCTCLPGWEGTNCETINIDECASPCMNGLGCLVDQVN 652	
QY 650 SYKICISDGEVAGYACETNINDCSNPCHNGGTCRDVLNDYFCDCKNGMKGTCHSRDSQC 709	
DB 653 SYVCFCLPGFTGHCETIDECASPLCLNGGQCLDRVDSYECVCAAGYAVRQCINIDEC 712	
QY 710 DEATCNNGGTCYDGDGAFKCMCPGGWGTTCNIARNSSCLPNPCHNGGTCV--VNGSFT 767	
DB 713 ASAPCQNGGVCDGVNGVYVCNAPGYTGDNCE-TEIDECASMPCLNGGACIEMWNG--YT 769	
QY 768 CVCKEGHEGPICAQNTNDSCPHPCVNSGTCDGVNMYRCECAPGAPGDCRININECOSS 827	
DB 770 CQCAGYTGVTICETDIDECASAPCQNGGVCVTDITNGYICACVPFTGSNCETNIDECASD 829	
QY 828 PCAFGATCVDIEINGVRCVPPGHGAKQOEVS-----GRPCITMGSVIPDGAKWDDCNT 882	
DB 830 PCLNGGICVDGVNGVFCQCPNYSGTYC-EISLDACRSMFQNGATCVNMGADY-----V 883	
QY 883 CQCLNGRIACSKVMCGPRPCLLHKHSECPGQSGSCIPILDDQCFVHPCTGVGECRSSLQ 942	
DB 884 CECVPGY-----AGQNC-EIDINECASLPQNGGLC-IDGIA 918	

QY 943 PVKTKCTSDSYQDNCANITF 963	
DB 919 GYTQCQRL-GYIGVNCCEEVGF 938	
RESULT 14	
S45306	
C;Species: Mus musculus (house mouse)	
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004	
C;Accession: S45306	
R;Lardelli, M.; Dahlstrand, J.; Lendahl, U.	
Mech. Dev. 46, 123-136, 1994	
A;Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-	
A;Reference number: S45306; MUID: 95001556; PMID: 7918057	
A;Accession: S45306	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-2318 <LAR>	
A;Cross-references: UNIPROT:Q61982; UNIPARC:UPI00002930C; EMBL:X74760; NID:G483580; PIN:	
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology	
F;163-195/Domain: EGF homology <EGF1>	
F;474-505/Domain: EGF homology <EGF>	
F;854-885/Domain: EGF homology <EGF2>	
F;1839-1871/Domain: ankyrin repeat homology <AN1>	
F;1872-1904/Domain: ankyrin repeat homology <AN2>	
F;1906-1938/Domain: ankyrin repeat homology <AN3>	
F;1939-1971/Domain: ankyrin repeat homology <AN4>	
F;1972-2004/Domain: ankyrin repeat homology <AN5>	
Query Match 23.7%; Score 1481.5; DB 2; Length 2318;	
Best Local Similarity 28.3%; Pred. No. 1.3e-77;	
Matches 319; Conservative 128; Mismatches 328; Indels 351; Gaps 35;	
QY 220 CMBGWMGPECN-RAICRQGCSPKHGSK---LPG----DRCQYQWQGLYC---DKCIPH 268	
DB 68 CLPGWGERCOLEDPCDHSGPCAGRGVCSQSSWAGTARFSCRLRGFCQGPDCSQPDPQVSR 127	
QY 269 PGCVHGI-C-----NEPWOCLCETNWGGQLCDKDLNCGTHQPCCLNGGTCSTNTPDKYQCS 323	
DB 128 P-CVHGAPCVGPDGRFACACPPGYQGSQSCSIDECRSTGTCRHGGTCLNT-PGSRQC 185	
QY 324 CPBGYSPNCEIAEHAACLSDPCHNRGSKETS-LGFECEGSPGWTGPTCTNIDDCSPNN 382	
DB 186 CPJGYTGLLCENVPWPCAPSPCRNGGTCROSSDYVDACLPGEFGQCNVNDVDCPGRH 245	
QY 383 CSHGTCQDLVNGFKVCVPPQWTKTCTOLDANECEAKP---CVNAKSKNLIASYCDCLP 440	
DB 246 CLNGGTCVDGVNTYNCQCPPEWTQFCTEDVDCEQLQPNACHNGGTCFNLLGGHSCVCVN 305	
QY 441 GWMQNCIDININDCL----- 455	
DB 306 GWTGESCSQNIIDDCATAVCFHGATCHDRVASFYCACPMGKTGLLCHLDDACVSNPCHEDA 365	
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DB 366 ICTNPNVSGRAICTCPGFTGGACDDQDVDECSIGANPCEHLGRCVNTQGSFLCCGRGT 425	
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DB 426 GPRCETDVNECLSGPCRNQATCLDRIGQFTICIMAGFTGYTCEVDIDECQSSPCVNGGVC 485	
QY 503 QNEINRFQCLCPTGFGSGLNCQLDIDYCEPNPQNGAACVYNRASYFCCKPEDEYEGKNCSH 562	
DB 486 KDRVNGFSCTCPGSGFSGMQCLDVDECASTPCRNGAKCVDPQDGYECRABGFGTLCER 545	
QY 563 LKHCRITPC-----EVIDSCTVAMASNDTPGVRYYIS-----SNVCGPHGKCKSQSG 610	
DB 546 NVDDCSFPDCHGRCVDGIASFSCACAPGYT--GIRCESQVDECRSPCRVGGKCLDLV- 602	
QY 611 GKFTCDCKGFTGYCHENINDCESNPCRNGGTCIDGVNSYKICISDGEVAGYACETNIND 670	
DB 603 DKVLCRCPGPTGVNCEVNIDDCASNPC-TFGVCRDGINRYDCVQCQPGFTGPLCNVINE 661	



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 4, 2006, 09:35:44 ; Search time 52 Seconds  
(without alignments)  
1696.441 Million cell updates/sec

Title: US-10-650-650-18

Perfect score: 6248

Sequence: 1 MRSPTRGSRPLSLALL.....LIAVAEVRQRPLKNRTD 1067

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : IssuedPatentSeqs\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6248	100.0	1067	2	US-09-579-536C-18
2	6248	100.0	1218	2	US-08-882-046-2
3	6248	100.0	1218	2	US-09-068-740A-11
4	6248	100.0	1218	2	US-09-566-047-2
5	6248	100.0	1218	2	US-09-579-536C-1
6	6248	100.0	1218	2	US-09-949-016-5902
7	6248	100.0	1254	2	US-09-949-016-10297
8	6241	99.9	1218	2	US-09-917-254-85
9	6233	99.8	1218	1	US-08-400-159-6
10	6233	99.8	1218	2	US-08-611-729A-6
11	6233	99.8	1218	2	US-09-195-524-6
12	6233	99.8	1218	2	US-09-310-685-4
13	6228	99.7	1218	2	US-09-214-278-7
14	6228	99.7	1218	2	US-09-855-722-7
15	6176	98.8	1208	2	US-09-199-865-1
16	6176	98.8	1208	2	US-10-213-329-1
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21	5969	95.5	1010	2	US-08-882-046-7
22	5969	95.5	1010	2	US-09-566-047-7
23	5466.5	87.5	1193	1	US-08-400-159-10
24	5466.5	87.5	1193	2	US-08-611-729A-10
25	5466.5	87.5	1193	2	US-09-195-524-10
26	5466.5	87.5	1193	2	US-09-310-685-8
27	3675	58.8	1238	2	US-09-214-278-5

28	3675	58.8	1238	2	US-09-855-722-5	Sequence 5, Appli
29	3662	58.6	1212	2	US-09-214-278-3	Sequence 3, Appli
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32	3654	58.5	1055	2	US-09-855-722-2	Sequence 2, Appli
33	3631.5	58.1	1248	2	US-08-882-046-6	Sequence 6, Appli
34	3631.5	58.1	1248	2	US-09-566-047-6	Sequence 6, Appli
35	3346	53.6	1148	2	US-08-882-046-4	Sequence 4, Appli
36	3346	53.6	1148	2	US-09-566-047-4	Sequence 4, Appli
37	3291	52.7	1065	1	US-08-400-159-8	Sequence 8, Appli
38	3287	52.6	1257	2	US-08-611-729A-8	Sequence 8, Appli
39	3287	52.6	1257	2	US-09-195-524-8	Sequence 8, Appli
40	3287	52.6	1257	2	US-09-310-685-6	Sequence 6, Appli
41	2339.5	37.4	1404	1	US-08-400-159-2	Sequence 2, Appli
42	2339.5	37.4	1404	2	US-08-611-729A-2	Sequence 2, Appli
43	2339.5	37.4	1404	2	US-09-195-524-2	Sequence 2, Appli
44	1585.5	25.4	2523	1	US-08-185-432-18	Sequence 18, Appli
45	1585.5	25.4	2523	2	US-08-899-232-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-579-536C-18

; Sequence 18, Application US/09579536C

; Patent No. 6716974

; GENERAL INFORMATION:

; APPLICANT: MACIAG, Thomas

; APPLICANT: ZIMRIN, Ann

; APPLICANT: SWALL, Deena

; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG

; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE: 053689-5002-01

; CURRENT APPLICATION NUMBER: US/09/579,536C

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/199,865

; PRIOR FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: PCT/US97/09407

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: US 60/018,841

; PRIOR FILING DATE: 1996-05-31

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 18

; LENGTH: 1067

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-579-536C-18

Query Match 100.0%; Score 6248; DB 2; Length 1067;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MRSPTRGSRPLSLALLCALRAKVCAGSGQFEILSMQNVGELQNGCCGARN	60
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Db	61	PGDRKCTRDECDYFKVCLKEYOSRVTAGGCPGSGSTVIGGNTFNKASRGNDNRRI	120
Qy	121	VLPFSFAWPRSYTLVVEAWDSNDTVQPSIIIEKASHSGMINPSROWOTLKQNTGVAHFE	180
Db	121	VLPFSFAWPRSYTLVVEAWDSNDTVQPSIIIEKASHSGMINPSROWOTLKQNTGVAHFE	180
Qy	181	YQIRVTCDYYGFGCNKFCRPRDDFFGHYACDQNGKTCMEGMGPECNRAICRQCSP	240
Db	181	YQIRVTCDYYGFGCNKFCRPRDDFFGHYACDQNGKTCMEGMGPECNRAICRQCSP	240
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301 GTHPCLNGGTCNTGPDKYQCSPEGYSGPNCIEAHACLSDPCPNRSGCKTSLGFEC 360  
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1021 IRDGNPIKEITDKIIDLKSRKDNSSLIAAVAEVRVQRRLKNRTD 1067  
1021 IRDGNPIKEITDKIIDLKSRKDNSSLIAAVAEVRVQRRLKNRTD 1067

RESULT 2  
US-08-882-046-2  
Sequence 2, Application US/08882046  
Patent No. 6136952  
GENERAL INFORMATION:  
APPLICANT: Li, Linheng  
APPLICANT: Hood, Leroy  
APPLICANT: Krantz, Ian D.  
APPLICANT: Spinner, Nancy B.  
TITLE OF INVENTION: Human Jagged Polypeptide, Encoding  
TITLE OF INVENTION: Nucleic Acids and Methods of Use  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA

ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,046  
FILING DATE: 25-JUN-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UW 2637  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1218 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-882-046-2  
Query Match 100.0%; Score 6248; DB 2; Length 1218;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 121 VLPFSFAWPSRYTLLEAVDSSNDTVQPDSSI EKASHGMINPSROWOTLKONTGVAHFE 180  
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DB 181 YQIRVTCDYDYYFGNKNFCRPRDDFFGHYACDQNGNKT CMEGWMGPECNRAICRQCSP 240  
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DB 241 KHGSKLPGDCRCQYGHQGLYCDKCIHPGCVHGI CNEPWQCLCETNMGSQLCDKDLNYC 300  
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1021 IRDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRPLKNRTD 1067

## RESULT 3

US-09-068-740A-11  
; Sequence 11, Application US/09068740A  
; Patent No. 637387  
; GENERAL INFORMATION:  
; APPLICANT: SAKANO, SEIJI  
; APPLICANT: ITOH, AKIRA  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8447  
; CURRENT APPLICATION NUMBER: US/09/068,740A  
; CURRENT FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: JP 7-299611  
; PRIOR FILING DATE: 1995-11-17  
; PRIOR APPLICATION NUMBER: JP 7-311811  
; PRIOR FILING DATE: 1995-11-30  
; PRIOR APPLICATION NUMBER: PCT/JP96/03356  
; PRIOR FILING DATE: 1996-11-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 1218  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-068-740A-11

Query Match 100.0%; Score 6248; DB 2; Length 1218;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MRSFRTGRSGRPLSLILLALCALRAKVCASGQFELEILSMQNVANGELONGCCGARN 60  
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61 PGRDKTRDCDITYFKVCLKEYOSRVTAGPCFSGSGTPIVIGNTFNLKASRGNDRRI 120  
121 VLPFSFAWPSRYTLLEAWDSSNDTVPQDSIIIEKASHSGMINPSRQWTLKQNTGVAHFE 180  
121 VLPFSFAWPSRYTLLEAWDSSNDTVPQDSIIIEKASHSGMINPSRQWTLKQNTGVAHFE 180  
181 YQIRVTCDDYYFGCNKFCRPRDDPFHGVACDQNGKTCMEGWMGPECNRAICROGCSP 240  
181 YQIRVTCDDYYFGCNKFCRPRDDPFHGVACDQNGKTCMEGWMGPECNRAICROGCSP 240

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961 ITFTFNKEMMSPGLTTEHICSELRLNMLKNVSAEYSIYIACBPPSPANNHVAISAED 1020  
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1021 IRDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRPLKNRTD 1067

## RESULT 4

US-09-566-047-2  
; Sequence 2, Application US/09566047  
; Patent No. 6703198  
; GENERAL INFORMATION:

APPLICANT: Li, Linheng  
Hood, Leroy  
Krantz, Ian D.  
Spinner, Nancy B.

TITLE OF INVENTION: Methods of Diagnosing Alagille Syndrome  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego

STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/566,047  
FILING DATE: 05-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/882,046  
FILING DATE: 25-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UW 4164  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (858) 535-9001  
TELEFAX: (858) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1218 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-566-047-2  
  
Query Match 100.0%; Score 6248; DB 2; Length 1218;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MRSPTGRGRPLSLALLCALRAKVCAGSGOFLEILSMQNVGELONGNCCGARN 60  
Db 1 MRSPTGRGRPLSLALLCALRAKVCAGSGOFLEILSMQNVGELONGNCCGARN 60  
  
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Db 61 PGDRKTRDECDTYFKVCLKEYQSRVTAGGCPSPGSGSTPVIGNTFNLKASGRNDRNI 120  
  
Qy 121 VLPSPFAPWPSYTLVLEAWSSNDTVQDPSIIIEKASHGMINPSRQWTLKONTGVAAFE 180  
Db 121 VLPSPFAPWPSYTLVLEAWSSNDTVQDPSIIIEKASHGMINPSRQWTLKONTGVAAFE 180  
  
Qy 181 YQIRVTCDYVYFGCNKFCRPRDDFGHYACDQNGNKTCEGWMGPECNRAICRQGCSP 240  
Db 181 YQIRVTCDYVYFGCNKFCRPRDDFGHYACDQNGNKTCEGWMGPECNRAICRQGCSP 240  
  
Qy 241 KHGSKCLPGDCRCQYGMGLYCDKCIPIHPGCVHIGICNEPWQCLCETNMGGLCDKDLNYC 300  
Db 241 KHGSKCLPGDCRCQYGMGLYCDKCIPIHPGCVHIGICNEPWQCLCETNMGGLCDKDLNYC 300  
  
Qy 301 GTHQPCPLNGTCSNTGPKYQCSPEGYSNGNCIAEHACLSDPCHNRGSKETSLGFEK 360  
Db 301 GTHQPCPLNGTCSNTGPKYQCSPEGYSNGNCIAEHACLSDPCHNRGSKETSLGFEK 360  
  
Qy 361 ECSPGWGTGPTCSNTIDDCSPNCSHGTCQDLVNGFKVCPPQWTGKTCQLDANECAKP 420  
Db 361 ECSPGWGTGPTCSNTIDDCSPNCSHGTCQDLVNGFKVCPPQWTGKTCQLDANECAKP 420  
  
Qy 421 CVNAKSKNLIASYCDCLPGMWGQNCNDINIDCLGQCONDASCRDLVNGYRCICPPGYA 480  
Db 421 CVNAKSKNLIASYCDCLPGMWGQNCNDINIDCLGQCONDASCRDLVNGYRCICPPGYA 480  
  
Qy 481 GDHCERDIDECASNPLNGHCQNEINRFQCLCPTGFSGNICOLDIDYCEPNQNGAQC 540  
Db 481 GDHCERDIDECASNPLNGHCQNEINRFQCLCPTGFSGNICOLDIDYCEPNQNGAQC 540  
  
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Db 541 YNRASDYFCKPEDYEGKNCSHLKHCRTPCEVIDSCVTAMASNDTPEGVRYISSNVCG 600

Db 541 YNRASDYFCKPEDYEGKNCSHLKHCRTPCEVIDSCVTAMASNDTPEGVRYISSNVCG 600  
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Db 601 PHGCKXSQSGGKFTCDNKGFTGTYCHENINDCESNPCRNGGTCIDGVNSYKICISDGE 660  
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Qy 721 YDEGDAFKCMCPGWEGETTCNIARNSSCLPNPCHNGGTCVNVNGESFTVCCKEGWEGPICA 780  
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Db 781 QNTNDCSPHPCYNSGTCVGDGNWYRCCEAGFAGPDCRININECQSSPCAFGATCVDEIN 840  
Qy 841 GYRCVCPPGHSGAKCOEVSGRPCITWGSVIPDCAKWDCCNTCQCLNGRIACSKVMCGPR 900  
Db 841 GYRCVCPPGHSGAKCOEVSGRPCITWGSVIPDCAKWDCCNTCQCLNGRIACSKVMCGPR 900  
Qy 901 PCLLKHGSHSECPGSGQSCIPILDDQCFVHPCTGVGECRSSSLQPVKTKTSDSYQDNCAN 960  
Db 901 PCLLKHGSHSECPGSGQSCIPILDDQCFVHPCTGVGECRSSSLQPVKTKTSDSYQDNCAN 960  
Qy 961 ITFTFNKEMMSPLGTTHEHCSELNLIKNVSAEYSIYIACBPSANNEIHVAISAED 1020  
Db 961 ITFTFNKEMMSPLGTTHEHCSELNLIKNVSAEYSIYIACBPSANNEIHVAISAED 1020  
Qy 1021 IRDGNPIKEITDKIIDLVSKRDGNSSLIAAAVAEVRVQRPLKNRTD 1067  
Db 1021 IRDGNPIKEITDKIIDLVSKRDGNSSLIAAAVAEVRVQRPLKNRTD 1067  
  
RESULT 5  
US-09-579-536C-1  
; Sequence 1, Application US/09579536C  
; Patent No. 6716974  
; GENERAL INFORMATION:  
; APPLICANT: MACIAG, Thomas  
; APPLICANT: ZIMRIN, Ann  
; APPLICANT: SMALL, Deena  
; APPLICANT: PRUDOVSKY, Igor  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG  
; FILE REFERENCE: 053689-5002-01  
; CURRENT APPLICATION NUMBER: US/09/579,536C  
; CURRENT FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/199,865  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: PCT/US97/09407  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/018,841  
; PRIOR FILING DATE: 1996-05-31  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 1218  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-579-536C-1  
  
Query Match 100.0%; Score 6248; DB 2; Length 1218;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MRSPTGRGRPLSLALLCALRAKVCAGSGOFLEILSMQNVGELONGNCCGARN 60  
Db 1 MRSPTGRGRPLSLALLCALRAKVCAGSGOFLEILSMQNVGELONGNCCGARN 60  
  
Qy 61 PGDRKTRDECDTYFKVCLKEYQSRVTAGGCPSPGSGSTPVIGNTFNLKASGRNDRNI 120  
Db 61 PGDRKTRDECDTYFKVCLKEYQSRVTAGGCPSPGSGSTPVIGNTFNLKASGRNDRNI 120  
  
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Db 121 VLPSPFAPWPSYTLVLEAWSSNDTVQDPSIIIEKASHGMINPSRQWTLKONTGVAAFE 180  
  
Qy 181 YQIRVTCDYVYFGCNKFCRPRDDFGHYACDQNGNKTCEGWMGPECNRAICRQGCSP 240  
Db 181 YQIRVTCDYVYFGCNKFCRPRDDFGHYACDQNGNKTCEGWMGPECNRAICRQGCSP 240  
  
Qy 241 KHGSKCLPGDCRCQYGMGLYCDKCIPIHPGCVHIGICNEPWQCLCETNMGGLCDKDLNYC 300  
Db 241 KHGSKCLPGDCRCQYGMGLYCDKCIPIHPGCVHIGICNEPWQCLCETNMGGLCDKDLNYC 300  
  
Qy 301 GTHQPCPLNGTCSNTGPKYQCSPEGYSNGNCIAEHACLSDPCHNRGSKETSLGFEK 360  
Db 301 GTHQPCPLNGTCSNTGPKYQCSPEGYSNGNCIAEHACLSDPCHNRGSKETSLGFEK 360  
  
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Db 361 ECSPGWGTGPTCSNTIDDCSPNCSHGTCQDLVNGFKVCPPQWTGKTCQLDANECAKP 420  
  
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Db 421 CVNAKSKNLIASYCDCLPGMWGQNCNDINIDCLGQCONDASCRDLVNGYRCICPPGYA 480  
  
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Db 541 YNRASDYFCKPEDYEGKNCSHLKHCRTPCEVIDSCVTAMASNDTPEGVRYISSNVCG 600

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Qy 121 VLPFSFAPRPSYTLLEAVDSSNDTVQPSDIIIEKASHSGMINFSPRQWTLKQNTGVAAHFE 180  
Db 121 VLPFSFAPRPSYTLLEAVDSSNDTVQPSDIIIEKASHSGMINFSPRQWTLKQNTGVAAHFE 180  
Qy 181 YQIRVTCDDYYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMPGECNRAICROGCSP 240  
Db 181 YQIRVTCDDYYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMPGECNRAICROGCSP 240  
Qy 241 KHGSKCLPGBRCQYQWQGLYCDKCIHPHGCVHGINENPQCLCETNMGQQLCDKDLNYC 300  
Db 241 KHGSKCLPGBRCQYQWQGLYCDKCIHPHGCVHGINENPQCLCETNMGQQLCDKDLNYC 300  
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Db 301 GTHQPCPLNGGTCSTNTGDKYQCSCEGYSGPNCIEAIEHAACLSDPCHNRGSKETSGLFEC 360  
Qy 361 ECSPGWGTGTCSTNIDDCSPNNSHGTCQDLVNGFKVCVCPQWTKTQOLDANECEAKP 420  
Db 361 ECSPGWGTGTCSTNIDDCSPNNSHGTCQDLVNGFKVCVCPQWTKTQOLDANECEAKP 420  
Qy 421 CVNAKSKNLIASVYCDCLPGWQGLYCDKCIHPHGCVHGINENPQCLCETNMGQQLCDKDLNYC 480  
Db 421 CVNAKSKNLIASVYCDCLPGWQGLYCDKCIHPHGCVHGINENPQCLCETNMGQQLCDKDLNYC 480  
Qy 481 GDHCERDIDECASNPCPLNGGHCQNEINRFQCLCPTGFSGNLCQDIDYCEPNPCQNGAQC 540  
Db 481 GDHCERDIDECASNPCPLNGGHCQNEINRFQCLCPTGFSGNLCQDIDYCEPNPCQNGAQC 540  
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Db 541 YNRASDYFCKCPEDYEGKNCCHLKHCRTPPCVIDSCTVAMASNDTPPEGVRISSNVCG 600  
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Db 601 PHGCKKSQSGGKFTCDCKNGFTGTGTYCHENINDCESNPRNGGTCIDGVNSYKICSDGWE 660  
Qy 661 GAYCETNINDCSQNPCHNGGTCRDLYNDFYCDCKNGWKGTCHSRDSQCDDEATCNNGGTC 720  
Db 661 GAYCETNINDCSQNPCHNGGTCRDLYNDFYCDCKNGWKGTCHSRDSQCDDEATCNNGGTC 720  
Qy 721 YBEGDAFKMCPGCGWEGTTCNIAINSCLIPNCHNGGTCVNVGESFTVCVKEGWEPICA 780  
Db 721 YBEGDAFKMCPGCGWEGTTCNIAINSCLIPNCHNGGTCVNVGESFTVCVKEGWEPICA 780  
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Db 841 GYRCVCPGHSQAKQCEVSGRPTITWGSVITPDGAKWDDCNTCCQLNGRIACSKVWCGPR 900  
Qy 901 PCLLHGHSECPGSGQCIPIILDQCFVHPTGTGVBGRSSSLQPVTKTSDSYQNCAN 960  
Db 901 PCLLHGHSECPGSGQCIPIILDQCFVHPTGTGVBGRSSSLQPVTKTSDSYQNCAN 960  
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Db 961 ITFTFNKEMWSPGLTTHICSELRNLNKNVSAEYIYIACPPSPANNEIHVAISAED 1020  
Qy 1021 IRDDGNPIKEITDKIIDLVSKRDNSSLIAAVAEVRQRRPLKNRTD 1067  
Db 1021 IRDDGNPIKEITDKIIDLVSKRDNSSLIAAVAEVRQRRPLKNRTD 1067

## RESULT 6

US-09-949-016-5902  
; Sequence 5902, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5902  
; LENGTH: 1218  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-949-016-5902

Query Match 100.0%; Score 6248; DB 2; Length 1218;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSPTRGSRPLSLLLALLCALRAKVCASGQFLEILSMQNVGELONGNCCCGARN 60  
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Db 61 PGRKCTREDCDITYFKVCLKEYQSRVTAGPCSFSGSSTPVIGNTFNLKASRGNDRNI 120  
Qy 121 VLPFSFAPRPSYTLLEAVDSSNDTVQPSDIIIEKASHSGMINFSPRQWTLKQNTGVAAHFE 180  
Db 121 VLPFSFAPRPSYTLLEAVDSSNDTVQPSDIIIEKASHSGMINFSPRQWTLKQNTGVAAHFE 180  
Qy 181 YQIRVTCDDYYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMPGECNRAICROGCSP 240  
Db 181 YQIRVTCDDYYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMPGECNRAICROGCSP 240  
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Db 241 KHGSKCLPGBRCQYQWQGLYCDKCIHPHGCVHGINENPQCLCETNMGQQLCDKDLNYC 300  
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Qy 361 ECSPGWGTGTCSTNIDDCSPNNSHGTCQDLVNGFKVCVCPQWTKTQOLDANECEAKP 420  
Db 361 ECSPGWGTGTCSTNIDDCSPNNSHGTCQDLVNGFKVCVCPQWTKTQOLDANECEAKP 420  
Qy 421 CVNAKSKNLIASVYCDCLPGWQGLYCDKCIHPHGCVHGINENPQCLCETNMGQQLCDKDLNYC 480  
Db 421 CVNAKSKNLIASVYCDCLPGWQGLYCDKCIHPHGCVHGINENPQCLCETNMGQQLCDKDLNYC 480  
Qy 481 GDHCERDIDECASNPCPLNGGHCQNEINRFQCLCPTGFSGNLCQDIDYCEPNPCQNGAQC 540  
Db 481 GDHCERDIDECASNPCPLNGGHCQNEINRFQCLCPTGFSGNLCQDIDYCEPNPCQNGAQC 540  
Qy 541 YNRASDYFCKCPEDYEGKNCCHLKHCRTPPCVIDSCTVAMASNDTPPEGVRISSNVCG 600  
Db 541 YNRASDYFCKCPEDYEGKNCCHLKHCRTPPCVIDSCTVAMASNDTPPEGVRISSNVCG 600  
Qy 601 PHGCKKSQSGGKFTCDCKNGFTGTGTYCHENINDCESNPRNGGTCIDGVNSYKICSDGWE 660  
Db 601 PHGCKKSQSGGKFTCDCKNGFTGTGTYCHENINDCESNPRNGGTCIDGVNSYKICSDGWE 660  
Qy 661 GAYCETNINDCSQNPCHNGGTCRDLYNDFYCDCKNGWKGTCHSRDSQCDDEATCNNGGTC 720  
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QY 841 GYRCVCPGHSAGKQCVSRGPCITWGSVTPDGAKWDDCNTCQCLNGRIACSKVWCGPR 900
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QY 901 PCLLKHGSHSCPSQSCIPILDDQCFVHPCTGVGECRASSLQPVKTKTSDSYQDNCA 960
Db 901 PCLLKHGSHSCPSQSCIPILDDQCFVHPCTGVGECRASSLQPVKTKTSDSYQDNCA 960
QY 961 ITFTFNKEMMSPLTTEHICSELRLNMLKNVSAEYSIYIACPPSPANNEIHVAISAED 1020
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QY 1021 IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRRPLKNRTD 1067
Db 1021 IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRRPLKNRTD 1067

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; Sequence 10297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10297
; LENGTH: 1254
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10297

Query Match 100.0%; Score 6248; DB 2; Length 1254;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 97 PGDRKTRDECDTFFKVCLEKYQSRVTAGGCPSCFGSGSTPVGNTFNLKASRGNDNR 156
QY 121 VLPFSFAMPVSTLLVEAWDSSNDTVPQDSIIIEKASHSGMTNPSRQWOTLKQNTGVAHFE 180
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QY 181 YQIRVTCDYYVFGCNKFCRPRDDFFGHYACDQNGNKTCHMEGWPPECNRAICRQGCSP 240
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QY 241 KHGSKLPGDCRCQYGWGLYCDKICIPHPGCVHIGICNEPWOCLCETNMGGLCDKDLNYC 300
Db 277 KHGSKLPGDCRCQYGWGLYCDKICIPHPGCVHIGICNEPWOCLCETNMGGLCDKDLNYC 336
QY 301 GTHQPCLINGGTCSTNTGPDYQCSCEPGYSGPNCEIAEHAACLSDPCHNRGSKETSLSGFEC 360
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Db 397 ECSPGWTGTCSTNIDDCSPNNCSHGTCQDLVNGFKVCYCPQWTKTCTOLDANECEAKP 456
QY 421 CYNKASCKNLIAASYCDCLPGMWGQNCININDCLGOQNDASCRDLVNGYRCICPPGYA 480
Db 457 CYNKASCKNLIAASYCDCLPGMWGQNCININDCLGOQNDASCRDLVNGYRCICPPGYA 516
QY 481 GDCERDIDECASNPCLINGGHCHQNEINRFQCLCPTGFSGNLCOLDIDYCEPNPCQNGAQC 540
Db 517 GDCERDIDECASNPCLINGGHCHQNEINRFQCLCPTGFSGNLCOLDIDYCEPNPCQNGAQC 576
QY 541 YNRASYFCCKPBDYEGKNCCHLKHCRTPPCBEVIDSCIVAMASNDTPGVRVYISSNVCG 600
Db 577 YNRASYFCCKPBDYEGKNCCHLKHCRTPPCBEVIDSCIVAMASNDTPGVRVYISSNVCG 636
QY 601 PHGCKSKSGGKFTCDCKNGFTGTYCHENINDCESNPCRNGGTCIDGVNSYKICICSDGWE 660
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QY 661 GAYCETNINDCSQNPCHNGGTCRDVLNDFYCDCKNGWKGTCHSRDSQCDDEATCNGGTC 720
Db 697 GAYCETNINDCSQNPCHNGGTCRDVLNDFYCDCKNGWKGTCHSRDSQCDDEATCNGGTC 756
QY 721 YDEGDAFKCMCPGWEGETTCNIARNSSCLPNPCHNGGTCVVNGESFTVCCKEGWGPICA 780
Db 757 YDEGDAFKCMCPGWEGETTCNIARNSSCLPNPCHNGGTCVVNGESFTVCCKEGWGPICA 816
QY 781 QNTNDCSHPYCNSGTCVGDGNWYRCBAPGAGPDCRININECQSSPCAFGATCVDEIN 840
Db 817 QNTNDCSHPYCNSGTCVGDGNWYRCBAPGAGPDCRININECQSSPCAFGATCVDEIN 876
QY 841 GYRCVCPGHSAGKQCVSRGPCITWGSVTPDGAKWDDCNTCQCLNGRIACSKVWCGPR 900
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QY 901 PCLLKHGSHSCPSQSCIPILDDQCFVHPCTGVGECRASSLQPVKTKTSDSYQDNCA 960
Db 937 PCLLKHGSHSCPSQSCIPILDDQCFVHPCTGVGECRASSLQPVKTKTSDSYQDNCA 996
QY 961 ITFTFNKEMMSPLTTEHICSELRLNMLKNVSAEYSIYIACPPSPANNEIHVAISAED 1020
Db 997 ITFTFNKEMMSPLTTEHICSELRLNMLKNVSAEYSIYIACPPSPANNEIHVAISAED 1056
QY 1021 IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRRPLKNRTD 1067
Db 1057 IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRRPLKNRTD 1103
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RESULT 8
US-09-917-254-85
; Sequence 85, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-85
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Query Match		99.9%;	Score 6241;	DB 2;	Length 1218;	
Best Local Similarity		99.9%;	Pred. No. 0;			
Matches 1066;		Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
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DB	1	MRSPTRGRSGRPLSLALLCALRAKVCASQGFLEILSMONVANGELONGNCCGARN	60			
QY	61	PGDKCTRDECDTYFKVCLKEYQSRVTAGGPGCSFGSGSTPVIGNTFNLKASRGNDRRI	120			
DB	61	PGDKCTRDECDTYFKVCLKEYQSRVTAGGPGCSFGSGSTPVIGNTFNLKASRGNDRRI	120			
QY	121	VLPSFAWPRSYTLLEAVDSSNDTVPDSIIIEKASHGMINPSROWTLKONTGVAHFE	180			
DB	121	VLPSFAWPRSYTLLEAVDSSNDTVPDSIIIEKASHGMINPSROWTLKONTGVAHFE	180			
QY	181	YQIRVTCDYDYFGNCKFCRPRDDFFGHYACDQNGNKTCEMGWGPCNRAICROGCSP	240			
DB	181	YQIRVTCDYDYFGNCKFCRPRDDFFGHYACDQNGNKTCEMGWGPCNRAICROGCSP	240			
QY	241	KHGSKLPGDCRCQYGMQGLYDKCIPHPGCVHGINCNEPMQCLCETNWGQLCDKDLNYC	300			
DB	241	KHGSKLPGDCRCQYGMQGLYDKCIPHPGCVHGINCNEPMQCLCETNWGQLCDKDLNYC	300			
QY	301	GTHQPCINGTCSNTGDKYQCSPEGYSGPNCEIAHAHCLSDPCNHRGSKETSIGFEC	360			
DB	301	GTHQPCINGTCSNTGDKYQCSPEGYSGPNCEIAHAHCLSDPCNHRGSKETSIGFEC	360			
QY	361	ECSPGWTGPTCSNIDDCSPNNCSHGTCODLVNGKVCPCPQWTKTOLDANECEAKP	420			
DB	361	ECSPGWTGPTCSNIDDCSPNNCSHGTCODLVNGKVCPCPQWTKTOLDANECEAKP	420			
QY	421	CYNAKSKNLIASYCDCLPGWQNGQNDININDCLGQNDASCRDLVNGYRVCIPPGYA	480			
DB	421	CYNAKSKNLIASYCDCLPGWQNGQNDININDCLGQNDASCRDLVNGYRVCIPPGYA	480			
QY	481	GDHCERDIDECANPCLNGHCQNEINRFOCLPTGFSNLCQLDIDYCEPNPCQGAOC	540			
DB	481	GDHCERDIDECANPCLNGHCQNEINRFOCLPTGFSNLCQLDIDYCEPNPCQGAOC	540			
QY	541	YNRASDYFCCKPDEYEGKNSHLKHCRTTPCEVIDSCVTAMASNDTPEGVRISSNVCG	600			
DB	541	YNRASDYFCCKPDEYEGKNSHLKHCRTTPCEVIDSCVTAMASNDTPEGVRISSNVCG	600			
QY	601	PHGKCKSQSGKFTCDCKNGFTGTCHENINDCESNRCNGTCDIGVNSYKICSDGWE	660			
DB	601	PHGKCKSQSGKFTCDCKNGFTGTCHENINDCESNRCNGTCDIGVNSYKICSDGWE	660			
QY	661	GAYCETNINDCSQNPCHNGTCDRLVNDFYCDCKNGWKGTCHSRDSQDEATCNNGTC	720			
DB	661	GAYCETNINDCSQNPCHNGTCDRLVNDFYCDCKNGWKGTCHSRDSQDEATCNNGTC	720			
QY	721	YDEGDAFKMCPGWEFTTCNIARNSSCLNPNCHNGTCTVNGESTCTCYCKEWEPICA	780			
DB	721	YDEGDAFKMCPGWEFTTCNIARNSSCLNPNCHNGTCTVNGESTCTCYCKEWEPICA	780			
QY	781	QNTNDCSPHPCYNSGTCTVDGNNYRCECAPFAGPDCRININQCSPSCAFAGTCDVEIN	840			
DB	781	QNTNDCSPHPCYNSGTCTVDGNNYRCECAPFAGPDCRININQCSPSCAFAGTCDVEIN	840			
QY	841	GYRCVCPGSHGAKQEVSGRPCIITWGSVIPDGAQWDDCNTCQCLNGRIACSKVWCGPR	900			
DB	841	GYRCVCPGSHGAKQEVSGRPCIITWGSVIPDGAQWDDCNTCQCLNGRIACSKVWCGPR	900			
QY	901	PCLLHGHSCPCSGOSCIPLDDQCFVHPCTGVGBCRSSSLQPVTKTSDSYQNCAN	960			
DB	901	PCLLHGHSCPCSGOSCIPLDDQCFVHPCTGVGBCRSSSLQPVTKTSDSYQNCAN	960			
QY	961	ITFTFNKEMSPGLTTEHICSELRLNLIKNSAEYSIYIACPPSPSANNIEHVAISAED	1020			
DB	961	ITFTFNKEMSPGLTTEHICSELRLNLIKNSAEYSIYIACPPSPSANNIEHVAISAED	1020			
QY	1021	IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAAVAEVRVQRPLKNRD 1067				

RESULT 9

US-08-400-159-6  
; Sequence 6; Application US/08400159  
; Patent No. 5869282  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowitz, David  
; APPLICANT: Henrique, Domingos M.P.  
; APPLICANT: Lewis, Julian H.  
; APPLICANT: Myat, Anna M.  
; APPLICANT: Fleming, Robert J.  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Mann, Robert S.  
; APPLICANT: Gray, Grace E.  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE  
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/400,159  
; FILING DATE: 02-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7326-029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 990-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1218 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-400-159-6

Query Match		99.8%;	Score 6233;	DB 1;	Length 1218;	
Best Local Similarity		99.7%;	Pred. No. 0;			
Matches 1064;		Conservative	1;	Mismatches	2;	Indels 0; Gaps 0;
QY	1	MRSPTRGRSGRPLSLALLCALRAKVCASQGFLEILSMONVANGELONGNCCGARN	60			
DB	1	MRSPTRGRSGRPLSLALLCALRAKVCASQGFLEILSMONVANGELONGNCCGARN	60			
QY	61	PGDKCTRDECDTYFKVCLKEYQSRVTAGGPGCSFGSGSTPVIGNTFNLKASRGNDRRI	120			
DB	61	PGDKCTRDECDTYFKVCLKEYQSRVTAGGPGCSFGSGSTPVIGNTFNLKASRGNDRRI	120			
QY	121	VLPSFAWPRSYTLLEAVDSSNDTVPDSIIIEKASHGMINPSROWTLKONTGVAHFE	180			
DB	121	VLPSFAWPRSYTLLEAVDSSNDTVPDSIIIEKASHGMINPSROWTLKONTGVAHFE	180			
QY	181	YQIRVTCDYDYFGNCKFCRPRDDFFGHYACDQNGNKTCEMGWGPCNRAICROGCSP	240			
DB	181	YQIRVTCDYDYFGNCKFCRPRDDFFGHYACDQNGNKTCEMGWGPCNRAICROGCSP	240			
QY	241	KHGSKLPGDCRCQYGMQGLYDKCIPHPGCVHGINCNEPMQCLCETNWGQLCDKDLNYC	300			

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Db 241 KHGSKLPGDCRCQYGMQGLYCDKCIHPGCVHGCINPEWQCLCEITNWGSQLCDKOLNYC 300
Qy 301 GTHQPCPLNGGTCNTGPDKYQCSCEGYSNPCEIAEHAHCLSDPCPNRGSKETSLSGFEC 360
Db 301 GTHQPCPLNGGTCNTGPDKYQCSCEGYSNPCEIAEHAHCLSDPCPNRGSKETSLSGFEC 360
Qy 361 ECSPGWTGPTCSTNIDDCSNPNCSHGTCQDLVNGFKVCVPPQWTGKTCOLDANECEAKP 420
Db 361 ECSPGWTGPTCSTNIDDCSNPNCSHGTCQDLVNGFKVCVPPQWTGKTCOLDANECEAKP 420
Qy 421 CVNAKSKNLIASYCDCLPGWQGNCDININDCLGQCNDAASCRDLVNGYRCICPPGYA 480
Db 421 CVNAKSKNLIASYCDCLPGWQGNCDININDCLGQCNDAASCRDLVNGYRCICPPGYA 480
Qy 481 GDHCERDIDECASNPLNGHGCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQGAQC 540
Db 481 GDHCERDIDECASNPLNGHGCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQGAQC 540
Qy 541 YNRASDYFCCKPEDYEGKNCSHLKHCHRTTTPCEVIDSCTVMAASNDTPEGVRYISSNVCG 600
Db 541 YNRASDYFCCKPEDYEGKNCSHLKHCHRTTTPCEVIDSCTVMAASNDTPEGVRYISSNVCG 600
Qy 601 PHGCKKSQSGKFTCDCKNGFTGTGYCHENINDCESNPCRNGGTCIDGVNSYKICSDGWE 660
Db 601 PHGCKKSQSGKFTCDCKNGFTGTGYCHENINDCESNPCRNGGTCIDGVNSYKICSDGWE 660
Qy 661 GAYCETNINDCSQNPCHNGGTCRLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNNGGTC 720
Db 661 GAYCETNINDCSQNPCHNGGTCRLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNNGGTC 720
Qy 721 YDEGDAFKMCPGMEGTTCNIARNSCLNPNCHNGGTCVVGESFTVCCKEGWGPICA 780
Db 721 YDEGDAFKMCPGMEGTTCNIARNSCLNPNCHNGGTCVVGESFTVCCKEGWGPICA 780
Qy 781 QNTNDCSPHPCYNSGTCVGDGNWYRCECAPGAFGDCRININEQSSPCAFAGTCVDEIN 840
Db 781 QNTNDCSPHPCYNSGTCVGDGNWYRCECAPGAFGDCRININEQSSPCAFAGTCVDEIN 840
Qy 841 GYRCVCPGHSQAKQEVSGRPTCTGMSVTPDGAKWDDDCNTCQCLNGRIACSKVWCGPR 900
Db 841 GYRCVCPGHSQAKQEVSGRPTCTGMSVTPDGAKWDDDCNTCQCLNGRIACSKVWCGPR 900
Qy 901 PCLLKHGSHSECPSSQSCIPILDDQCFVHPCTGVGECRSSLSQPVKTKTSDSYQDNCAN 960
Db 901 PCLLKHGSHSECPSSQSCIPILDDQCFVHPCTGVGECRSSLSQPVKTKTSDSYQDNCAN 960
Qy 961 ITFTFNKEMWSPGLTTEHICSELRLNLIKNSVAEYSIYIACEPSPSANNIEHVAISAED 1020
Db 961 ITFTFNKEMWSPGLTTEHICSELRLNLIKNSVAEYSIYIACEPSPSANNIEHVAISAED 1020
Qy 1021 IRDGNPIKEITDKIIDLVSXRDGNSSLIAAVAEVRVQRRLKNRD 1067
Db 1021 IRDGNPIKEITDKIIDLVSXRDGNSSLIAAVAEVRVQRRLKNRD 1067
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## RESULT 10

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US-08-611-729A-6
; Sequence 6, Application US/08611729A
; Patent No. 6004924
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Teakonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace E.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; SERATE GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,729A
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1218 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-611-729A-6
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Query Match 99.8%; Score 6233; DB 2; Length 1218;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSPTRGSRPLSLALLCALRAKVCAGSQFEILEILSMQNVNGLQNGNCCGARN 60
Db 1 MRSPTRGSRPLSLALLCALRAKVCAGSQFEILEILSMQNVNGLQNGNCCGARN 60
Qy 61 PGDKCTRDECDYFVKCLKEYOSRVTAGGSPGSGSTPVIIGNTFNKASRNDNRNI 120
Db 61 PGDKCTRDECDYFVKCLKEYOSRVTAGGSPGSGSTPVIIGNTFNKASRNDNRNI 120
Qy 121 VLPFSFAWPRSYTLLEAVDSSNDTVQPSDIIIEKASHGMINFSRQWTLKQNTGVAHFE 180
Db 121 VLPFSFAWPRSYTLLEAVDSSNDTVQPSDIIIEKASHGMINFSRQWTLKQNTGVAHFE 180
Qy 181 YQIRVTCDDYYFGCNKFCRPRDDPFPHVACDQNGKTCMEGWMGPECNRAICROGCSP 240
Db 181 YQIRVTCDDYYFGCNKFCRPRDDPFPHVACDQNGKTCMEGWMGPECNRAICROGCSP 240
Qy 241 KHGSKLPGDCRCQYGMQGLYCDKCIHPGCVHGCINPEWQCLCEITNWGSQLCDKOLNYC 300
Db 241 KHGSKLPGDCRCQYGMQGLYCDKCIHPGCVHGCINPEWQCLCEITNWGSQLCDKOLNYC 300
Qy 301 GTHQPCPLNGGTCNTGPDKYQCSCEGYSNPCEIAEHAHCLSDPCPNRGSKETSLSGFEC 360
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Qy 361 ECSPGWTGPTCSTNIDDCSNPNCSHGTCQDLVNGFKVCVPPQWTGKTCOLDANECEAKP 420
Db 361 ECSPGWTGPTCSTNIDDCSNPNCSHGTCQDLVNGFKVCVPPQWTGKTCOLDANECEAKP 420
Qy 421 CVNAKSKNLIASYCDCLPGWQGNCDININDCLGQCNDAASCRDLVNGYRCICPPGYA 480
Db 421 CVNAKSKNLIASYCDCLPGWQGNCDININDCLGQCNDAASCRDLVNGYRCICPPGYA 480
Qy 481 GDHCERDIDECASNPLNGHGCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQGAQC 540
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Db 541 YNRASDYFCCKPEDYEGKNCSHLKHCHRTTTPCEVIDSCTVMAASNDTPEGVRYISSNVCG 600
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Db 541 YNRADYFCKPEDYEGKNCVSHLKHCHRTTCEVIDSCCTVAMASNDTPGVRYISSNVCG 600  
Qy 601 PHGCKSQSGKFTCDNKGFTGTGCHENINDCESNPCRNGGTGIDGVNSYKICSDGWE 660  
Db 601 PHGCKSQSGKFTCDNKGFTGTGCHENINDCESNPCRNGGTGIDGVNSYKICSDGWE 660  
Qy 661 GAYCETINDCSONPCHNGGTCRDVLVNDYFCDCKNGWKGTCHSRDSCQDEATCNGGTC 720  
Db 661 GAYCETINDCSONPCHNGGTCRDVLVNDYFCDCKNGWKGTCHSRDSCQDEATCNGGTC 720  
Qy 721 YDEGDAFKMCPGWEGTTCNIARNSSCLPNPCHNGGTCVNVGSEFTVCCKEGWGPICA 780  
Db 721 YDEGDAFKMCPGWEGTTCNIARNSSCLPNPCHNGGTCVNVGSEFTVCCKEGWGPICA 780  
Qy 781 QNTNDCSPHPCYNSGTCTVDGNWYRCBAPGADGCRININEQSSPCAFGATCVDEIN 840  
Db 781 QNTNDCSPHPCYNSGTCTVDGNWYRCBAPGADGCRININEQSSPCAFGATCVDEIN 840  
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Db 841 GYRCVCPGHSKACQEVSGRPCITMGSVIPDGAKWDDDCNTCQCLNGRIACSKVWCGPR 900  
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Db 901 PCLLKHGSECPGSCQICPILDDQCFVHPCTGVGECRSSIOPVKTCTSDSYQDNCAN 960  
Qy 961 ITFTFNKEMSPGLTTEHICSELNMLNKVSAEYSIYIACEPSPSANNHIVHSAED 1020  
Db 961 ITFTFNKEMSPGLTTEHICSELNMLNKVSAEYSIYIACEPSPSANNHIVHSAED 1020  
Qy 1021 IRDGNPIKEITDKIIDLVSQRDGNSSLIAAVAVRVRPLKVRTD 1067  
Db 1021 IRDGNPIKEITDKIIDLVSQRDGNSSLIAAVAVRVRPLKVRTD 1067

## RESULT 11

US-09-195-524-6  
; Sequence 6, Application US/09195524  
; Patent No. 6703489  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos M. P.  
; APPLICANT: Lewis, Julian H.  
; APPLICANT: Myat, Anna M.  
; APPLICANT: Fleming, Robert J.  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Mann, Robert S.  
; APPLICANT: Gray, Grace E.  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE  
; TITLE OF INVENTION: SRRATE GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/195,524  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; FILING DATE: 06-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 7326-037  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1218 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; US-09-195-524-6

Query Match 99.8%; Score 6233; DB 2; Length 1218;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1064; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSPTTRGRGRPLSLALLCALRAKVCASGOFELEILSMQNVNGLONGNCCGARN 60  
Db 1 MRSPTTRGRGRPLSLALLCALRAKVCASGOFELEILSMQNVNGLONGNCCGARN 60  
Qy 61 PGRKCTTRDCDITYFKVCLKEYQSRVTAGGPCSGSGSTPVIIGNTFNLKASRNDNR 120  
Db 61 PGRKCTTRDCDITYFKVCLKEYQSRVTAGGPCSGSGSTPVIIGNTFNLKASRNDNR 120  
Qy 121 VLPFSFAPWPSRYTLLEAVDSSNDTVQPSDIIIEKASHSGMINPSRQWOTLKQNTGVAHFE 180  
Db 121 VLPFSFAPWPSRYTLLEAVDSSNDTVQPSDIIIEKASHSGMINPSRQWOTLKQNTGVAHFE 180  
Qy 181 YQIRVTCDDYYGFGCNKFCRPRDDPFHYACDQNGKTCMEGWMPGECNRAICROQCS 240  
Db 181 YQIRVTCDDYYGFGCNKFCRPRDDPFHYACDQNGKTCMEGWMPGECNRAICROQCS 240  
Qy 241 KHGSKLPGRDRCQYGMQGLYCDKCIHPGCVHGI CNEPQCICETNMGQOLCDKLDNYC 300  
Db 241 KHGSKLPGRDRCQYGMQGLYCDKCIHPGCVHGI CNEPQCICETNMGQOLCDKLDNYC 300  
Qy 301 GTHQPCNLNGGTCNTGPDKYQCSCEPGYSGPNCIEAHEACLSDPCHNRSGCKETS LGFEC 360  
Db 301 GTHQPCNLNGGTCNTGPDKYQCSCEPGYSGPNCIEAHEACLSDPCHNRSGCKETS LGFEC 360  
Qy 361 ECSPGWTGTCSTNIDDCSPNNSHGTCQDLVNGFKVCVPPQWTGTCOLDANECAKP 420  
Db 361 ECSPGWTGTCSTNIDDCSPNNSHGTCQDLVNGFKVCVPPQWTGTCOLDANECAKP 420  
Qy 421 CVNAKSKNLIASYCDCLPGWNGQCDININDCLGQCONDASCRDLVNGYRCICPPGYA 480  
Db 421 CVNAKSKNLIASYCDCLPGWNGQCDININDCLGQCONDASCRDLVNGYRCICPPGYA 480  
Qy 481 GDHCERDIDECASNPCNLNGGHCQNEINRFQCLCPTGFSNLCQLDIDYCEPNPCQNGAQC 540  
Db 481 GDHCERDIDECASNPCNLNGGHCQNEINRFQCLCPTGFSNLCQLDIDYCEPNPCQNGAQC 540  
Qy 541 YNRADYFCKPEDYEGKNCVSHLKHCHRTTCEVIDSCCTVAMASNDTPGVRYISSNVCG 600  
Db 541 YNRADYFCKPEDYEGKNCVSHLKHCHRTTCEVIDSCCTVAMASNDTPGVRYISSNVCG 600  
Qy 601 PHGCKSQSGKFTCDNKGFTGTGCHENINDCESNPCRNGGTGIDGVNSYKICSDGWE 660  
Db 601 PHGCKSQSGKFTCDNKGFTGTGCHENINDCESNPCRNGGTGIDGVNSYKICSDGWE 660  
Qy 661 GAYCETINDCSONPCHNGGTCRDVLVNDYFCDCKNGWKGTCHSRDSCQDEATCNGGTC 720  
Db 661 GAYCETINDCSONPCHNGGTCRDVLVNDYFCDCKNGWKGTCHSRDSCQDEATCNGGTC 720  
Qy 721 YDEGDAFKMCPGWEGTTCNIARNSSCLPNPCHNGGTCVNVGSEFTVCCKEGWGPICA 780  
Db 721 YDEGDAFKMCPGWEGTTCNIARNSSCLPNPCHNGGTCVNVGSEFTVCCKEGWGPICA 780  
Qy 781 QNTNDCSPHPCYNSGTCTVDGNWYRCBAPGADGCRININEQSSPCAFGATCVDEIN 840  
Db 781 QNTNDCSPHPCYNSGTCTVDGNWYRCBAPGADGCRININEQSSPCAFGATCVDEIN 840

QY 841 GYRCVCPGSHGAKCOEVSGRPCITMGSVIPDGAkWDDDCNTCQCLNGRIACSKVWGCPR 900  
DB 841 GYRCVCPGSHGAKCOEVSGRPCITMGSVIPDGAkWDDDCNTCQCLNGRIACSKVWGCPR 900  
QY 901 PCLLKHGSHSCPSQSCIPILDQCFVHPCTGVGECRSSLQPVKTKTSDSYQDNCAN 960  
DB 901 PCLLKHGSHSCPSQSCIPILDQCFVHPCTGVGECRSSLQPVKTKTSDSYQDNCAN 960  
QY 961 ITFTFNKEMMSPLTTEHICSELRLNLIKNVSAEYSIYIACBSPSANNHVAISAED 1020  
DB 961 ITFTFNKEMMSPLTTEHICSELRLNLIKNVSAEYSIYIACBSPSANNHVAISAED 1020  
QY 1021 IRDDGNPIKEITDKIIDLVSQRDGNSSLIAAVAEVRVQRPLKNRTD 1067  
DB 1021 IRDDGNPIKEITDKIIDLVSQRDGNSSLIAAVAEVRVQRPLKNRTD 1067

RESULT 12  
US-09-310-685-4  
; Sequence 4, Application US/09310685  
; Patent No. 6887475  
; GENERAL INFORMATION:  
; APPLICANT: Lamb, Jonathan R  
; APPLICANT: Dallman, Margaret J  
; APPLICANT: Hoyne, Gerard F  
; TITLE OF INVENTION: No. 6887475ch  
; FILE REFERENCE: 674525-2001  
; CURRENT APPLICATION NUMBER: US/09/310,685  
; CURRENT FILING DATE: 1999-05-04  
; PRIOR APPLICATION NUMBER: GB 9623236.8  
; PRIOR FILING DATE: 1996-11-07  
; PRIOR APPLICATION NUMBER: GB 9715674.9  
; PRIOR FILING DATE: 1997-07-24  
; PRIOR APPLICATION NUMBER: GB 9719350.2  
; PRIOR FILING DATE: 1997-09-11  
; PRIOR APPLICATION NUMBER: PCT/GB97/03058  
; PRIOR FILING DATE: 1997-11-06  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 1218  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-310-685-4

Query Match 99.8%; Score 6233; DB 2; Length 1218;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1064; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRSRTRGRSGRPLSLLLALLCALRAKVCAGSGOFLEILSMQNVNGLQNGCCGGARN 60  
DB 1 MRSRTRGRSGRPLSLLLALLCALRAKVCAGSGOFLEILSMQNVNGLQNGCCGGARN 60  
QY 61 PGDRKCTREDCDTYFKVCLKEYQSRVTAGGCPSCFGSGSTPVIGGNTFNLKASRGNDRNRI 120  
DB 61 PGDRKCTREDCDTYFKVCLKEYQSRVTAGGCPSCFGSGSTPVIGGNTFNLKASRGNDRNRI 120  
QY 121 VLPSFAWPRSYTLIVAEWDSNDTVQDPSIIEKASHSGMINPSRQWTLKONTGVVAHFE 180  
DB 121 VLPSFAWPRSYTLIVAEWDSNDTVQDPSIIEKASHSGMINPSRQWTLKONTGVVAHFE 180  
QY 181 YQIRVTCDYYGFGCNKFCPRDDFGHYACDQNGKNTCEGWMGPECNRAICRQGCSP 240  
DB 181 YQIRVTCDYYGFGCNKFCPRDDFGHYACDQNGKNTCEGWMGPECNRAICRQGCSP 240  
QY 241 KHGSKLPGDCRCQYGMWGLYCDKICPHPGCVHGI CNEPWQCLCETNWWGGLCDKLDNYC 300  
DB 241 KHGSKLPGDCRCQYGMWGLYCDKICPHPGCVHGI CNEPWQCLCETNWWGGLCDKLDNYC 300  
QY 301 GTHQPLNGGTCNTGPDYKQCSPEBYSGNPCETAEHACLSDPCHNRGSKCTSLGPEC 360  
DB 301 GTHQPLNGGTCNTGPDYKQCSPEBYSGNPCETAEHACLSDPCHNRGSKCTSLGPEC 360

QY 361 ECSPGWTGPTCSTNIDDCSPNNCSHGCTQDVLNFGFKVCPPQMTGKTCOLDANECEAKP 420  
DB 361 ECSPGWTGPTCSTNIDDCSPNNCSHGCTQDVLNFGFKVCPPQMTGKTCOLDANECEAKP 420  
QY 421 CVNAKCKNLIASYYCDCLPGWNGQNCNINDCLGQCCQNDASCRDLVNGYRCICPPGYA 480  
DB 421 CVNAKCKNLIASYYCDCLPGWNGQNCNINDCLGQCCQNDASCRDLVNGYRCICPPGYA 480  
QY 481 GDHCERDIDECASNPCLINGHCQNEINRFQCLCPTGFSNLCOLDIDYCEPNPCQNGAQC 540  
DB 481 GDHCERDIDECASNPCLINGHCQNEINRFQCLCPTGFSNLCOLDIDYCEPNPCQNGAQC 540  
QY 541 YNRASDYFKCPEDEYEGKNCNHLKDHCRFTTPCEVIDSCVTAMASNDTPEGVRYISSNVCG 600  
DB 541 YNRASDYFKCPEDEYEGKNCNHLKDHCRFTTPCEVIDSCVTAMASNDTPEGVRYISSNVCG 600  
QY 601 PHGKCKSQSGGKFTCDCKNGFTGTYCHENINDCESNPCRNGGTCIDGVNSYKICSDGWE 660  
DB 601 PHGKCKSQSGGKFTCDCKNGFTGTYCHENINDCESNPCRNGGTCIDGVNSYKICSDGWE 660  
QY 661 GAYCETNINDCSNPCHNGGTCRDVLNDFYCDCKNGWKGTCHSRDSQCDDEATCNGGTC 720  
DB 661 GAYCETNINDCSNPCHNGGTCRDVLNDFYCDCKNGWKGTCHSRDSQCDDEATCNGGTC 720  
QY 721 YDEGDAFKCMCPGSGWEGTTCNIARNSSCLPNPCHNGGTCVNVGESFTVCCKEGWEGPICA 780  
DB 721 YDEGDAFKCMCPGSGWEGTTCNIARNSSCLPNPCHNGGTCVNVGESFTVCCKEGWEGPICA 780  
QY 781 QNTNDCSPHPCYNSGTCVGDNDWYRECAPGAPDCRININECQSSPCAFGATCVDEN 840  
DB 781 QNTNDCSPHPCYNSGTCVGDNDWYRECAPGAPDCRININECQSSPCAFGATCVDEN 840  
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DB 841 GYRCVCPGSHGAKCOEVSGRPCITMGSVIPDGAkWDDDCNTCQCLNGRIACSKVWGCPR 900  
QY 901 PCLLKHGSHSCPSQSCIPILDQCFVHPCTGVGECRSSLQPVKTKTSDSYQDNCAN 960  
DB 901 PCLLKHGSHSCPSQSCIPILDQCFVHPCTGVGECRSSLQPVKTKTSDSYQDNCAN 960  
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DB 961 ITFTFNKEMMSPLTTEHICSELRLNLIKNVSAEYSIYIACBSPSANNHVAISAED 1020  
QY 1021 IRDDGNPIKEITDKIIDLVSQRDGNSSLIAAVAEVRVQRPLKNRTD 1067  
DB 1021 IRDDGNPIKEITDKIIDLVSQRDGNSSLIAAVAEVRVQRPLKNRTD 1067

RESULT 13  
US-09-214-278-7  
; Sequence 7, Application US/09214278  
; Patent No. 6291210  
; GENERAL INFORMATION:  
; APPLICANT: Sakano, Seiji  
; APPLICANT: Itoh, Akira  
; TITLE OF INVENTION: DIPPERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8576  
; CURRENT APPLICATION NUMBER: US/09/214,278  
; CURRENT FILING DATE: 1999-01-26  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1218  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-214-278-7

Query Match 99.7%; Score 6228; DB 2; Length 1218;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1065; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRSRTRGRSGRPLSLLLALLCALRAKVCAGSGOFLEILSMQNVNGLQNGCCGGARN 60

[illegible]

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US-09-855-722-7
; Sequence 7, Application US/09855722
; Patent No. 6638741
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itch, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-722-7

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Query Match          99.7%; Score 6228; DB 2; Length 1218;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1065: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db	1	MRS	PRTGR	SGRPL	SLLL	LALL	CAL	RAK	VC	GA	SQ	FE	IL	SM	QNV	NG	EL	QNC	CG	GARN	60							
Qy	61	PGD	KCTR	DECD	TF	FKV	CL	KEY	QSR	VT	AG	GC	PS	FG	SG	TP	VI	GN	TF	NL	KAS	RGN	DR	NR	120			
Db	61	PGD	KCTR	DESD	TF	FKV	CL	KEY	QSR	VT	AG	GC	PS	FG	SG	TP	VI	GN	TF	NL	KAS	RGN	DR	NR	120			
Qy	121	VL	PS	FA	WPS	Y	TLL	VE	AW	SS	ND	T	Q	P	D	S	I	I	E	K	A	S	H	S	GM	180		
Db	121	VL	PS	FA	WPS	Y	TLL	VE	AW	SS	ND	T	Q	P	D	S	I	I	E	K	A	S	H	S	GM	180		
Qy	181	YQ	IR	VT	CDD	Y	Y	Y	Y	Y	Y	G	C	N	K	F	R	P	R	D	D	F	F	G	H	Y	240	
Db	181	YQ	IR	VT	CDD	Y	Y	Y	Y	Y	Y	G	C	N	K	F	R	P	R	D	D	F	F	G	H	Y	240	
Qy	241	KH	G	S	C	L	P	G	D	C	R	C	O	Y	G	H	O	G	L	Y	C	D	K	C	I	P	H	300
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Qy	361	E	C	S	P	G	T	G	P	T	C	S	T	N	I	D	C	S	P	N	N	C	S	H	G	G	T	420
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Qy	481	G	D	H	C	E	R	D	I	D	E	C	A	S	N	P	C	L	G	H	G	H	C	O	N	E	I	540
Db	481	G	D	H	C	E	R	D	I	D	E	C	A	S	N	P	C	L	G	H	G	H	C	O	N	E	I	540
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Qy	601	P	H	G	K	C	S	Q	S	G	K	F	T	C	D	C	N	K	G	F	T	G	Y	C	H	E	N	660
Db	601	P	H	G	K	C	S	Q	S	G	K	F	T	C	D	C	N	K	G	F	T	G	Y	C	H	E	N	660
Qy	661	G	A	C	E	T	N	I	N	D	C	S	O	N	P	C	H	N	G	T	C	R	D	L	V	N	D	720
Db	661	G	A	C	E	T	N	I	N	D	C	S	O	N	P	C	H	N	G	T	C	R	D	L	V	N	D	720
Qy	721	Y	D	E	G	A	P	K	M	C	P	G	G	E	G	T	T	C	N	I	A	R	N	S	C	L	P	780

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Db 721 YDEGAFKCPGWEGETTCNIARNSSCLNPNCHNGGTCTVNGESFTVCCKEWEGPICA 780
Qy 781 QNTNDCSPHPCYNSTGTCVGDGNWYRCAPFAGPDCRININECQSSPCAFGATCVDDEIN 840
Db 781 QNTNDCSPHPCYNSTGTCVGDGNWYRCAPFAGPDCRININECQSSPCAFGATCVDDEIN 840
Qy 841 GYRCVCPGHSAGAKQCVSRGPCITMGSVIPDGAKWDDDCNTCQCLNGRIACSKWCGPR 900
Db 841 GYRCVCPGHSAGAKQCVSRGPCITMGSVIPDGAKWDDDCNTCQCLNGRIACSKWCGPR 900
Qy 901 PCLLKHGSHSEPCSQSCIPILDDQCFVHPCTGVGECRSSLSLPQVTKTSDSYQDNMCAN 960
Db 901 PCLLKHGSHSEPCSQSCIPILDDQCFVHPCTGVGECRSSLSLPQVTKTSDSYQDNMCAN 960
Qy 961 ITFTFNKEMMSPGLTTEHICSELRLNMLKNVSAEYSIYIACEPSPSANNEIHVAISAED 1020
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Qy 1021 IRDDGNPIKEITDKIIDLVSKRDNSSLIAAVAEVRVORRPLKNRTD 1067
Db 1021 IRDDGNPIKEITDKIIDLVSKRDNSSLIAAVAEVRVORRPLKNRTD 1067

RESULT 15
US-09-199-865-1
; Sequence 1, Application US/09199865
; Patent No. 6433138
; GENERAL INFORMATION:
; APPLICANT: Zimrin, Ann B.
; APPLICANT: Maciag, Thomas
; APPLICANT: Wong, Michael K.K.
; APPLICANT: Pepper, Michael S.
; APPLICANT: Montesano, Roberto
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS
; TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 0036-1U1
; CURRENT APPLICATION NUMBER: US/09/199,865
; CURRENT FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: 60/018,841
; EARLIER FILING DATE: 1996-05-31
; EARLIER APPLICATION NUMBER: PCT/US97/09407
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-199-865-1

Query Match 98.8%; Score 6176; DB 2; Length 1208;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1054; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GRPLSLLLALICARAKVCGASGQFELIILSMQNVNGBELQNGCCGARNPDGRKCTRDE 70
Db 1 GTSLSLLLLALICARAKVCGASGQFELIILSMQNVNGBELQNGCCGARNPDGRKCTRDE 60

Qy 71 CDTYFKVCLKEYQSVRTAGGPCSGSGSTPVTGGNTFNLKASRGNDNRNIVLPFSFAWPR 130
Db 61 CDTYFKVCLKEYQSVRTAGGPCSGSGSTPVTGGNTFNLKASRGNDNRNIVLPFSFAWPR 120

Qy 131 SYTLIVEAWDSSNDTVQSDSIIEKASHSGMINPSRQWOTLKQNTGVAHFYQIRVTCDDY 190
Db 121 SYTLIVEAWDSSNDTVQSDSIIEKASHSGMINPSRQWOTLKQNTGVAHFYQIRVTCDDY 180

Qy 191 YYGFCNKFCDPRDDFFGHYACDQNGKTCHEGWMGPCNRAICRQGSPKHGSKCLPGD 250
Db 181 YYGFCNKFCDPRDDFFGHYACDQNGKTCHEGWMGPCNRAICRQGSPKHGSKCLPGD 240

Qy 251 CRCQYGMQGLYCDKCIPIHPGCVHGI CNEPWQCLCETNMGQQLCDKDLNYCGTHQPCLINGG 310
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Db 241 CRCQYGMQGLYCDKCIPIHPGCVHGI CNEPWQCLCETNMGQQLCDKDLNYCGTHQPCLINGG 300
Qy 311 TCSNTGPDKYQCSCEPGYSGPNCEIAEHACLSDPCHNRGCKETSIGFPECSPGWTGPT 370
Db 301 TCSNTGPDKYQCSCEPGYSGPNCEIAEHACLSDPCHNRGCKETSIGFPECSPGWTGPT 360
Qy 371 CSTNIDDCSPNNCSHGCTQDILVNGFKVCVCPPOWTGKTQOLDANECEAKPCVNAKSCNKL 430
Db 361 CSTNIDDCSPNNCSHGCTQDILVNGFKVCVCPPOWTGKTQOLDANECEAKPCVNAKSCNKL 420
Qy 431 IASYYCDCLPGMWGQNCIDININDCLQCCQNDASCRDLVNGYRCICPPGVAGDHCEERDIDE 490
Db 421 IASYYCDCLPGMWGQNCIDININDCLQCCQNDASCRDLVNGYRCICPPGVAGDHCEERDIDE 480
Qy 491 CASNPCLNGHCHQNEINRFQCLCPTGFSGNLCOLDIDYCEPNPCQNGAQCYNRASDYFCK 550
Db 481 CASNPCLNGHCHQNEINRFQCLCPTGFSGNLCOLDIDYCEPNPCQNGAQCYNRASDYFCK 540
Qy 551 CPEDYEGKNCSHLKHCRTPPCVIDSDCTVAMASNDTPPEGVYISSNVCGPHGCKKSQSG 610
Db 541 CPEDYEGKNCSHLKHCRTPPCVIDSDCTVAMASNDTPPEGVYISSNVCGPHGCKKSQSG 600
Qy 611 GKFTCDNKGFTCTYCHENINDCESNCRNGGTCIDGVNSYKICISDGMWEGAYCETNIND 670
Db 601 GKFTCDNKGFTCTYCHENINDCESNCRNGGTCIDGVNSYKICISDGMWEGAYCETNIND 660
Qy 671 CSQNPCHNGGTCRDLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNGGTCYDGDGAFKCM 730
Db 661 CSQNPCHNGGTCRDLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNGGTCYDGDGAFKCM 720
Qy 731 CPGWEGTTCNIARNSSCLNPNCHNGGTCVNGESFTVCCKEWEGPICANTINDCSPPH 790
Db 721 CPGWEGTTCNIARNSSCLNPNCHNGGTCVNGESFTVCCKEWEGPICANTINDCSPPH 780
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Db 841 SGAKCQEVSRGPCITMGSVIPDGAKWDDDCNTCQCLNGRIACSKWCGPRPCLLKHGSHSE 900
Qy 911 CPSSQSCIPILDDQCFVHPCTGVGECRSSLSLPQVTKTSDSYQDNMCANITFTFNKEMM 970
Db 901 CPSSQSCIPILDDQCFVHPCTGVGECRSSLSLPQVTKTSDSYQDNMCANITFTFNKEMM 960
Qy 971 SPGLTTEHICSELRLNMLKNVSAEYSIYIACEPSPSANNEIHVAISAEDIRDDGNPIKE 1030
Db 961 SPGLTTEHICSELRLNMLKNVSAEYSIYIACEPSPSANNEIHVAISAEDIRDDGNPIKE 1020
Qy 1031 ITDKIIDLVSKRDNSSLIAAVAEVRVORRPLKNRTD 1067
Db 1021 ITDKIIDLVSKRDNSSLIAAVAEVRVORRPLKNRTD 1057
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Search completed: February 4, 2006, 09:37:26

Job time : 56 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 4, 2006, 09:27:34 ; Search time 271 Seconds  
(without alignments)  
2777.855 Million cell updates/sec

Title: US-10-650-650-18

Perfect score: 6248

Sequence: 1 MESPRTGRSGRPLSLALL.....LIAVAENVQRPLKNRFTD 1067

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6248	100.0	1218	1 JAG1_HUMAN	P78504 homo sapien
2	6239	99.9	1218	2 Q4KMR2_HUMAN	Q4KMR2 homo sapien
3	6089	97.5	1219	1 JAG1_RAT	Q63722 rattus norv
4	6086	97.4	1218	1 JAG1_MOUSE	Q9QXX0 mus musculu
5	5469.5	87.5	1193	2 Q90819_CHICK	Q90819 gallus gall
6	5263	84.2	1214	2 Q90YD2_XENLA	Q90YD2 xenopus lae
7	5225	83.6	1051	2 Q5U4U1_XENLA	Q5U4U1 xenopus lae
8	4768.5	76.3	1213	1 JAG1B_BRARE	Q90Y54 brachydanio
9	4505.5	72.1	1242	1 JAG1A_BRARE	Q90Y57 brachydanio
10	4293.5	68.7	1364	2 Q4RQ03_TETNG	Q4RQ03 tetraodon n
11	3985	63.8	1212	2 Q42347_CHICK	Q42347 gallus gall
12	3795.5	60.7	1254	2 Q90Y56_BRARE	Q90Y56 brachydanio
13	3790.5	60.7	1254	2 Q5TZX8_BRARE	Q5TZX8 brachydanio
14	3789.5	60.7	1254	2 Q9YHU2_BRARE	Q9YHU2 brachydanio
15	3685	59.0	1238	1 JAG2_HUMAN	Q9Y219 homo sapien
16	3656	58.5	1247	1 JAG2_MOUSE	Q9QY65 mus musculu
17	3590.5	57.5	1216	2 Q90Y55_BRARE	Q90Y55 brachydanio
18	3585.5	57.4	1216	2 Q5TZX7_BRARE	Q5TZX7 brachydanio
19	3557.5	56.9	1202	1 JAG2_RAT	P97607 rattus norv
20	3174	50.8	1128	2 Q4SG68_TETNG	Q4SG68 tetraodon n
21	2923	46.8	1477	2 Q4H3A4_CIOIN	Q4H3A4 ciona intes
22	2335.5	37.4	1404	1 SERR_DROME	P18168 drosophila
23	2040.5	32.7	950	2 Q8MQN5_DROME	Q8MQN5 drosophila
24	1982.5	31.7	932	2 Q7Q867_ANOGA	Q7Q867 anopheles g
25	1585.5	25.4	2524	1 NOTCH_XENLA	P21783 xenopus lae
26	1584	25.4	2428	2 Q8I6X6_BOOMI	Q8I6X6 boophilus m
27	1582	25.3	2602	2 Q7PSV8_ANOGA	Q7PSV8 anopheles g
28	1580.5	25.3	2703	1 NOTCH_DROME	P07207 drosophila
29	1569.5	25.1	2528	2 Q8AXP0_CYNPY	Q8AXP0 cynops pyrr
30	1567	25.1	2471	1 NOTC2_HUMAN	Q04721 homo sapien
31	1567	25.1	2471	2 Q5VTD0_HUMAN	Q5VTD0 homo sapien

32	1562	25.0	2471	1 NOTC2_RAT	Q9QW30 rattus norv
33	1560	25.0	2555	2 Q5SXM3_HUMAN	Q5SXM3 homo sapien
34	1556	24.9	1235	2 Q6IQ50_HUMAN	Q6IQ50 homo sapien
35	1555	24.9	2437	1 NOTC1_BRARE	P46530 brachydanio
36	1554.5	24.9	713	2 Q962W9_PODCA	Q962W9 podocoryne
37	1552	24.8	2531	2 Q7TQ50_MOUSE	Q7TQ50 mus musculu
38	1551	24.8	2531	2 Q8K428_MOUSE	Q8K428 mus musculu
39	1549	24.8	2531	1 NOTC1_MOUSE	Q01705 mus musculu
40	1548	24.8	2653	2 Q25253_LUCCU	Q25253 lucilia cup
41	1544.5	24.7	2516	2 Q7TQ52_MOUSE	Q7TQ52 mus musculu
42	1544.5	24.7	2526	2 Q7TQ51_MOUSE	Q7TQ51 mus musculu
43	1543	24.7	2470	1 NOTC2_MOUSE	Q35516 mus musculu
44	1541.5	24.7	2556	1 NOTC1_HUMAN	P46531 homo sapien
45	1538.5	24.6	2531	1 NOTC1_RAT	Q07008 rattus norv

#### ALIGNMENTS

RESULT 1  
JAG1\_HUMAN  
ID JAG1\_HUMAN STANDARD; PRT; 1218 AA.  
AC P78504; O14902; O15122; Q15816;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE Jagged-1 precursor (Jagged1) (hJ1).  
OS Name=JAG1; Synonyms=JAGL1;  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=97422615; PubMed=9268641; DOI=10.1006/geno.1997.4820;  
RA Oda T., Elkahlon A.G., Meltzer P.S., Chandrasekharappa S.C.;  
RT "Identification and cloning of the human homolog (JAG1) of the rat Jagged1 gene from the Alagille syndrome critical region at 20p12.";  
RL Genomics 43:376-379(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT AGS CVS-184.  
RC TISSUE=Bone marrow;  
RX MEDLINE=97351506; PubMed=9207788;  
RA Li L., Krantz I.D., Deng Y., Genin A., Banta A.B., Collins C.C.,  
RA Qi M., Traak B.J., Kuo W.L., Cochran J., Costa T., Pierpont M.E.M.,  
RA Rand E.B., Piccoli D.A., Hood L., Spinner N.B.;  
RT "Alagille syndrome is caused by mutations in human Jagged1, which encodes a ligand for Notch1.";  
RL Nat. Genet. 16:243-251(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.  
RX MEDLINE=98122342; PubMed=9462510; DOI=10.1016/S1074-7613(00)80457-4;  
RA Li L., Wilner L.A., Deng Y., Iwata M., Banta A.B., Graf L.,  
RA Marcovina S., Friedman C., Traak B.J., Hood L., Torok-Storb B.;  
RT "The human homolog of rat Jagged1 expressed by marrow stroma inhibits differentiation of 32D cells through interaction with Notch1.";  
RL Immunity 8:43-55(1998).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Cervical carcinoma;  
RX MEDLINE=99262417; PubMed=10329626; DOI=10.1093/emboj/18.10.2803;  
RA Bash J., Zong W.-X., Banga S., Rivera A., Ballard D.W., Ron Y.,  
RA Gelinis C.;  
RT "Rel/NF-kappaB can trigger the Notch signaling pathway by inducing the expression of Jagged1, a ligand for Notch receptors.";  
RL EMBO J. 18:2803-2811(1999).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=99180765; PubMed=10079256;  
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.;  
RT "Human ligands of the Notch receptor.";

- Am. J. Pathol. 154:785-794(1999).
- [6]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RP MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
RX Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
RA Bailey J.P., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,  
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Lehaeslao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showlken R., Sims S.,  
RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sultston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.B., Whittaker P., Willey D.B., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
Rogers J.;  
RP "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).
- [7]  
RN NUCLEOTIDE SEQUENCE [MRNA] OF 14-1218.  
RP TISSUE=Unilateral vein endothelial cell;  
RX MEDLINE=97115768; PubMed=8955070; DOI=10.1074/jbc.271.51.32499;  
RA Zimin A.B., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,  
RA Maciag T.;  
RP "An antisense oligonucleotide to the notch ligand jagged enhances  
RT fibroblast growth factor-induced angiogenesis in vitro.";  
RL J. Biol. Chem. 271:32499-32502(1996).
- [8]  
RN DISEASE.  
RP MEDLINE=97351505; PubMed=9207787;  
RX Oda T., Elkahloun A.G., Pike B.L., Okajima K., Krantz I.D., Genin A.,  
RA Piccoli D.A., Meltzer P.S., Spinner N.B., Collins F.S.,  
RA Chandrasekharappa S.C.;  
RP "Mutations in the human Jagged1 gene are responsible for Alagille  
RT syndrome.";  
RL Nat. Genet. 16:235-242(1997).
- [9]  
RN DEVELOPMENTAL STAGE.  
RP MEDLINE=20436345; PubMed=10978356; DOI=10.1136/jmg.37.9.658;  
RX Jones E.A., Clement-Jones M., Wilson D.I.;  
RA "Jagged1 expression in human embryos: correlation with the Alagille  
RT syndrome phenotype.";  
RL J. Med. Genet. 37:663-668(2000).
- [10]  
RN VARIANTS AGS CYS-184 AND HIS-184.  
RP MEDLINE=98254456; PubMed=9585603;  
RX Krantz I.D., Colliton R.P., Genin A., Rand E.B., Li L., Piccoli D.A.,  
RA Spinner N.B.;  
RP "Spectrum and frequency of jagged1 (JAG1) mutations in Alagille  
RT syndrome patients and their families.";  
RL Am. J. Hum. Genet. 62:1361-1369(1998).
- [11]  
RN VARIANTS AGS HIS-79; THR-127; ARG-129; LEU-163; GLY-184; SER-187;  
RP GLY-229; PHE-284; CYS-288; PHE-438; SER-731 AND ARG-740.  
RX MEDLINE=99239888; PubMed=10220506;  
RA Croenier C., Driancourt C., Raynaud N., Dhorne-Pollet S., Pollet N.,  
RA Bernard O., Hadchouel M., Meunier-Rotival M.;  
RP "Mutations in JAGGED1 gene are predominantly sporadic in Alagille  
RT syndrome.";  
RL Gastroenterology 116:1141-1148(1999).
- [12]  
RN VARIANTS AGS THR-152 AND LEU-184.  
RP MEDLINE=20004539; PubMed=10533065;  
RX DOI=10.1002/(SICI)1098-1004(199911)14:5<394::AID-HUMU5>3.0.CO;2-1;  
RA Filia G., Uda M., Macis D., Frau F., Cripponi L., Balli F.,  
RA Barbera C., Colombo C., Frediani T., Gatti R., Iorio R., Marazzi M.G.,  
RA Marcellini M., Musumeci S., Nebbia G., Vajro P., Ruffa G., Zancan L.,  
RA Cao A., Devigilis S.;  
RP "Jagged-1 mutation analysis in Italian Alagille syndrome patients.";  
RL Hum. Mutat. 14:394-400(1999).
- [13]  
RN VARIANTS AGS TYR-229 AND ARG-386.  
RP MEDLINE=20514559; PubMed=11058898;  
RX DOI=10.1002/1098-1004(200011)16:5<408::AID-HUMU5>3.0.CO;2-9;  
RA Heritage M.L., MacMillan J.C., Colliton R.P., Genin A., Spinner N.B.,  
RA Anderson G.J.;  
RP "Jagged1 (JAG1) mutation detection in an Australian Alagille syndrome  
RT population.";  
RL Hum. Mutat. 16:408-416(2000).
- [14]  
RN VARIANT TOP ASP-274.  
RP MEDLINE=21067871; PubMed=11152664; DOI=10.1093/hmg/10.2.163;  
RX Eldadah Z.A., Hamosh A., Biery N.J., Montgomery R.A., Duke M.,  
RA Etkins R., Dietz H.C.;  
RP "Familial Tetralogy of Fallot caused by mutation in the jagged1  
RT gene.";  
RL Hum. Mol. Genet. 10:163-169(2001).
- [15]  
RN VARIANT AGS SER-37.  
RP MEDLINE=21096916; PubMed=11157803; DOI=10.1093/hmg/10.4.405;  
RX Morrisette J.D., Colliton R.P., Spinner N.B.;  
RA "Defective intracellular transport and processing of JAG1 missense  
RT mutations in Alagille syndrome.";  
RL Hum. Mol. Genet. 10:405-413(2001).
- [16]  
RN VARIANTS AGS PHE-220 AND ARG-753.  
RP MEDLINE=20579880; PubMed=11139247;  
RX DOI=10.1002/1098-1004(2001)17:1<72::AID-HUMU11>3.0.CO;2-U;  
RA Croenier C., Driancourt C., Raynaud N., Hadchouel M.,  
RA Meunier-Rotival M.;  
RP "Fifteen novel mutations in the JAGGED1 gene of patients with Alagille  
RT syndrome.";  
RL Hum. Mutat. 17:72-73(2001).
- [17]  
RN FUNCTION: Ligand for multiple Notch receptors and involved in the  
RP mediation of Notch signaling. May be involved in cell-fate  
CC decisions during hematopoiesis. Seems to be involved in early and  
CC late stages of mammalian cardiovascular development. Inhibits  
CC myoblast differentiation (By similarity). Enhances fibroblast  
CC growth factor-induced angiogenesis (in vitro).  
CC -1- SUBUNIT: Interacts with NOTCH1, NOTCH2 and NOTCH3 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.  
CC In cervix epithelium expressed in undifferentiated subcolumnar  
CC reserve cells and squamous metaplasia. Expression is up-regulated  
CC in cervical squamous cell carcinoma. Expressed in bone marrow cell  
CC line HS-27a which supports the long-term maintenance of immature  
CC progenitor cells.  
CC -1- DEVELOPMENTAL STAGE: Expressed in 32-52 days embryos in the distal  
CC cardiac outflow tract and pulmonary artery, major arteries, portal  
CC vein, optic vesicle, otocyst, branchial arches, metanephros,  
CC pancreas, mesocardium, around the major bronchial branches, and in  
CC the neural tube.  
CC -1- DISEASE: Defects in JAG1 are the cause of Alagille syndrome (AGS)  
CC [MIM:118450]. AGS is an autosomal dominant developmental disorder  
CC that affects structures in the liver, heart, skeleton, eye, kidney  
CC and other organs.  
CC -1- DISEASE: Defects in JAG1 are a cause of tetralogy of Fallot (TOF)  
CC [MIM:187500]. TOF is a congenital heart anomaly which consists of  
CC pulmonary stenosis, ventricular septal defect, dextroposition of  
CC the aorta (aorta is on the right side instead of the left) and  
CC hypertrophy of the right ventricle. This condition results in a  
CC blue baby at birth due to inadequate oxygenation. Surgical  
CC correction is emergent.

```
CC -I- SIMILARITY: Contains 1 DSL domain.
CC -I- SIMILARITY: Contains 15 EGF-like domains.

Query Match      100.0%; Score 6248; DB 1; Length 1218;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1067; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSPTGRSGRPLSLALLCALRAKVCASQGFLEILSMQNVGELQNGCCGARN 60
DB 1 MRSPTGRSGRPLSLALLCALRAKVCASQGFLEILSMQNVGELQNGCCGARN 60

QY 61 PGDRKCTRDECDTFFVKCLKEYQSRVTAGPCSPGSGSTPVIGNTFNLKASRGNDRNRI 120
DB 61 PGDRKCTRDECDTFFVKCLKEYQSRVTAGPCSPGSGSTPVIGNTFNLKASRGNDRNRI 120

QY 121 VLPFSFAWPRSYTLLEAVDSSNDTVQPSIIIEKASHSGMINPSRQWTLKQNTGVVAHFE 180
DB 121 VLPFSFAWPRSYTLLEAVDSSNDTVQPSIIIEKASHSGMINPSRQWTLKQNTGVVAHFE 180

QY 181 YQIRVTCDDYYVYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMGPECNRAICROGCSP 240
DB 181 YQIRVTCDDYYVYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMGPECNRAICROGCSP 240

QY 241 KHGSKCLPGRCQYQWGLYCDKCIHPGCVHGI CNEPWQCLCETNMGGLCDKOLNYC 300
DB 241 KHGSKCLPGRCQYQWGLYCDKCIHPGCVHGI CNEPWQCLCETNMGGLCDKOLNYC 300

QY 301 GTHQPCPLNGTCSNTGPDYKQCSPEGYSPNCEIAEHACLSDPCHNRGSKETSGLGFE 360
DB 301 GTHQPCPLNGTCSNTGPDYKQCSPEGYSPNCEIAEHACLSDPCHNRGSKETSGLGFE 360

QY 361 ECSPGWTGPTCSNIDPCSPNCSHGTCQDLVNGFKVCYCPQWTKTQOLDANECEAKP 420
DB 361 ECSPGWTGPTCSNIDPCSPNCSHGTCQDLVNGFKVCYCPQWTKTQOLDANECEAKP 420

QY 421 CVNAKSKNLIASVYCDLPQWQNGQNDININCLGQNDASCRDLVNGYRCICPPGYA 480
DB 421 CVNAKSKNLIASVYCDLPQWQNGQNDININCLGQNDASCRDLVNGYRCICPPGYA 480

QY 481 GDHCERDIDECASNPLNGHGCQNEINRFQCLPTGFGNLCQLDIDYCEPNPCQNGAQC 540
DB 481 GDHCERDIDECASNPLNGHGCQNEINRFQCLPTGFGNLCQLDIDYCEPNPCQNGAQC 540

QY 541 YNRASDYFCKPDEYEGKNCNHLKHCRTPTPCEVIDCTVAMASNDTPEGVRISSNVCG 600
DB 541 YNRASDYFCKPDEYEGKNCNHLKHCRTPTPCEVIDCTVAMASNDTPEGVRISSNVCG 600

QY 601 PHGCKKSQSGKFTCDCKNGFTGTTCYCHENINDCESNPCRNGGTCIDGVNSYKICSDGWE 660
DB 601 PHGCKKSQSGKFTCDCKNGFTGTTCYCHENINDCESNPCRNGGTCIDGVNSYKICSDGWE 660

QY 661 GAYCETNINDCSQNPCHNGTCDRLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNGGTC 720
DB 661 GAYCETNINDCSQNPCHNGTCDRLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNGGTC 720

QY 721 YDEGDAFKMCPGWEETTCNIARNSSCLPNPCHNGTCTVVGESFTVCVKEGWEPICA 780
DB 721 YDEGDAFKMCPGWEETTCNIARNSSCLPNPCHNGTCTVVGESFTVCVKEGWEPICA 780

QY 781 QNTNDCSPHPCYNSGTCTVDGNNYRCBAPGAPGDCRININECOSQSPCAFGATCVDEN 840
DB 781 QNTNDCSPHPCYNSGTCTVDGNNYRCBAPGAPGDCRININECOSQSPCAFGATCVDEN 840

QY 841 GYRCVCPPHGSHGAKQCVSGRPTCTMGSVIPDGAkWDDCNTQCLNGRIACSKVWCGPR 900
DB 841 GYRCVCPPHGSHGAKQCVSGRPTCTMGSVIPDGAkWDDCNTQCLNGRIACSKVWCGPR 900

QY 901 PCLLKHGSHSPGSGQSCIPILDDQCFVHPCTGVGECSRSLQPVKTKTSDSYQDNCAN 960
DB 901 PCLLKHGSHSPGSGQSCIPILDDQCFVHPCTGVGECSRSLQPVKTKTSDSYQDNCAN 960

QY 961 ITFTFNKEMSPGLTTEHICSELRLNLIKVAEYSIYIACEPSPSANNIEHVAISAED 1020
DB 961 ITFTFNKEMSPGLTTEHICSELRLNLIKVAEYSIYIACEPSPSANNIEHVAISAED 1020

Db 961 ITFTFNKEMSPGLTTEHICSELRLNLIKVAEYSIYIACEPSPSANNIEHVAISAED 1020
QY 1021 IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRPLKNRTD 1067
DB 1021 IRDDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEVRVQRPLKNRTD 1067

RESULT 2
Q4KMR2 HUMAN
ID Q4KMR2 HUMAN PRELIMINARY; PRT; 1218 AA.
AC Q4KMR2;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Jagged 1.
GN Names=JAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC098393; AAB98393.1; -, mRNA.
SQ SEQUENCE 1218 AA; 133874 MW; 8E1E45A42253E5CB CRC64;

Query Match      99.9%; Score 6239; DB 2; Length 1218;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1066; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRSPTGRSGRPLSLALLCALRAKVCASQGFLEILSMQNVGELQNGCCGARN 60
DB 1 MRSPTGRSGRPLSLALLCALRAKVCASQGFLEILSMQNVGELQNGCCGARN 60

QY 61 PGDRKCTRDECDTFFVKCLKEYQSRVTAGPCSPGSGSTPVIGNTFNLKASRGNDRNRI 120
DB 61 PGDRKCTRDECDTFFVKCLKEYQSRVTAGPCSPGSGSTPVIGNTFNLKASRGNDRNRI 120

QY 121 VLPFSFAWPRSYTLLEAVDSSNDTVQPSIIIEKASHSGMINPSRQWTLKQNTGVVAHFE 180
DB 121 VLPFSFAWPRSYTLLEAVDSSNDTVQPSIIIEKASHSGMINPSRQWTLKQNTGVVAHFE 180

QY 181 YQIRVTCDDYYVYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMGPECNRAICROGCSP 240
DB 181 YQIRVTCDDYYVYFGCNKFCRPRDDFFGHYACDQNGKTCMEGWMGPECNRAICROGCSP 240
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QY 241 KHGSKCLPGDCRCQYQWGLYCDKCIHPGCVHGI CNEPWQCLCETNWGQOLCKDLNYC 300
Db 241 KHGSKCLPGDCRCQYQWGLYCDKCIHPGCVHGI CNEPWQCLCETNWGQOLCKDLNYC 300
QY 301 GTHQPCNLGGTCSNTGPDYKQCSCEGYSGPNCIEAHACLSDPCHNRGSKETSGLGFEC 360
Db 301 GTHQPCNLGGTCSNTGPDYKQCSCEGYSGPNCIEAHACLSDPCHNRGSKETSGLGFEC 360
QY 361 ECSFGWTGPTCSNIDDCSPNNCSHGTCQDLVNGFKVCVCPQWTKTQOLDANECEAKP 420
Db 361 ECSFGWTGPTCSNIDDCSPNNCSHGTCQDLVNGFKVCVCPQWTKTQOLDANECEAKP 420
QY 421 CVNAKSKNLIASYCDCLPGWQNGCDIINDCIGQCONDCASCRDLVNGYRGCIPPGYA 480
Db 421 CVNAKSKNLIASYCDCLPGWQNGCDIINDCIGQCONDCASCRDLVNGYRGCIPPGYA 480
QY 481 GDHCERDIDECASNPLCNGHGCQNEINRFQCLCPTGFGSNLCQLDIDYCEPNFCQGAQC 540
Db 481 GDHCERDIDECASNPLCNGHGCQNEINRFQCLCPTGFGSNLCQLDIDYCEPNFCQGAQC 540
QY 541 YNRASDYFCCKPEDYEGKNCNLSHLKDHCRTPPCVEIDSCIVAMASNDTPGVRVYISSNVC 600
Db 541 YNRASDYFCCKPEDYEGKNCNLSHLKDHCRTPPCVEIDSCIVAMASNDTPGVRVYISSNVC 600
QY 601 PHGCKKSQSGKFTCDCKNGKFTGTGTCHENINDCESNRCNGGTCIDGWSYKICSDGWE 660
Db 601 PHGCKKSQSGKFTCDCKNGKFTGTGTCHENINDCESNRCNGGTCIDGWSYKICSDGWE 660
QY 661 GAYCETNINDCSQNPCHNGGTCDRLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNNGGTC 720
Db 661 GAYCETNINDCSQNPCHNGGTCDRLVNDYFCDCKNGWKGTCHSRDSQCDDEATCNNGGTC 720
QY 721 YDEGDAFKCPCGWEGTTCNIARNSSCLNPNCHNGTCTVNGESFTVCYCKEGWEGPICA 780
Db 721 YDEGDAFKCPCGWEGTTCNIARNSSCLNPNCHNGTCTVNGESFTVCYCKEGWEGPICA 780
QY 781 QNTNDCSPHCYNSTGTCVGDNNVRCBAPGAPGDCRININECQSSPCAFAGATCVUDEIN 840
Db 781 QNTNDCSPHCYNSTGTCVGDNNVRCBAPGAPGDCRININECQSSPCAFAGATCVUDEIN 840
QY 841 GYRCVCPFGHSGAKQCVSRPCITMGSVIPDGAkWDDDCNTCQCLNGRIACSKVMCGPR 900
Db 841 GYRCVCPFGHSGAKQCVSRPCITMGSVIPDGAkWDDDCNTCQCLNGRIACSKVMCGPR 900
QY 901 PCLLKHGSECPQSGQCIPILDQCFVHPCTGVGECRSSLOPVKTKTSDSYQDNCAN 960
Db 901 PCLLKHGSECPQSGQCIPILDQCFVHPCTGVGECRSSLOPVKTKTSDSYQDNCAN 960
QY 961 ITFTFNKEMMSPGLTTEHICSELNMLNKNVSAEYIYIACEPSPSANNEIHVAISAED 1020
Db 961 ITFTFNKEMMSPGLTTEHICSELNMLNKNVSAEYIYIACEPSPSANNEIHVAISAED 1020
QY 1021 IRDGNPIKEITDKIIDLKVRKDNSSLIAAVAEVRVQRRLPKNRDT 1067
Db 1021 IRDGNPIKEITDKIIDLKVRKDNSSLIAAVAEVRVQRRLPKNRDT 1067

RESULT 3
JAG1 RAT
ID JAG1 RAT STANDARD; PRT; 1219 AA.
AC Q63722; P70640;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Jagged-1 precursor (Jagged1).
GN Name=Jagi;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

```
RC TISSUE=Sciatic nerve;
RX MEDLINE=95211842; PubMed=7697721; DOI=10.1016/0092-8674(95)90294-5;
RA Lindseell C.B., Shawber C.J., Boulter J., Weinmaster G.;
RT "Jagged: a mammalian ligand that activates Notch1.";
RL Cell 80:909-917(1995).
CC -1- FUNCTION: Ligand for multiple Notch receptors and involved in the
CC mediation of Notch signaling. May be involved in cell-fate
CC decisions during hematopoiesis. Enhances fibroblast growth factor-
CC induced angiogenesis (in vitro). Seems to be involved in early and
CC late stages of mammalian cardiovascular development. Inhibits
CC myoblast differentiation. May regulate fibroblast growth factor-
CC induced angiogenesis.
CC -1- SUBUNIT: Interacts with NOTCH1, NOTCH2 and NOTCH3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed in a variety of tissues.
CC -1- DEVELOPMENTAL STAGE: Expression is seen in E11.5-E14.5 embryos in
CC four distinct regions of the ventricular zone in the developing
CC spinal cord.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 15 EGF-like domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L38483; AAB06509.1; -, mRNA.
DR HSSP; P00740; 1EDM.
DR Ensembl; ENSRNOG00000007443; Rattus norvegicus.
DR RGD; 2937; Jag1.
DR GO; GO:0005576; C:extracellular region; ISS.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0008083; F:growth factor activity; ISS.
DR GO; GO:0005112; F:Notch binding; ISS.
DR GO; GO:0005198; F:structural molecule activity; ISS.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0001709; P:cell fate determination; NAS.
DR GO; GO:0045446; P:endothelial cell differentiation; ISS.
DR GO; GO:0030097; P:hemopoiesis; ISS.
DR GO; GO:0030216; P:keratinocyte differentiation; ISS.
DR GO; GO:0045445; P:myoblast differentiation; ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0042127; P:regulation of cell proliferation; ISS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca_bd.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR011651; MNML.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 11.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF07657; MNML; 1.
DR PRINTS; PR00010; EGFLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS01051; DSL_1.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS00026; EGF_3; 16.
DR PROSITE; PS01187; EGF_CA; 8.
KW Calcium; Developmental protein; EGF-like domain; Glycoprotein;
KW Notch signaling pathway; Repeat; Signal; Transmembrane.
FT SIGNAL 1 33 Potential.
FT CHAIN 34 1219 Jagged-1.
FT TOPO_DOM 34 1067 Extracellular (Potential).
FT TRANSMEM 1068 1093 Potential.
```

FT	TOPO_DOM	1094	1219	Cytoplasmic (Potential).	QY	1	MRSPTGRSGRPLSLALLCALRAKVCASQGFLEILSMQNVANGELQNGCCGARN	60
FT	DOMAIN	185	229	DSL.	QY	1		60
FT	DOMAIN	230	266	EGF-like 1; atypical.	Db	1		60
FT	DOMAIN	296	334	EGF-like 2.	Db	1		60
FT	DOMAIN	336	372	EGF-like 3.	QY	61	PGDKTRTRECPTYFKVCLKEYQSVRTAGGPCSGSTPVIGNTFNLKASGNDNRRI	120
FT	DOMAIN	374	410	EGF-like 4; calcium-binding (Potential).	QY	61		120
FT	DOMAIN	412	448	EGF-like 5; calcium-binding (Potential).	QY	61		120
FT	DOMAIN	450	485	EGF-like 6; calcium-binding (Potential).	QY	61		120
FT	DOMAIN	487	523	EGF-like 7; calcium-binding (Potential).	QY	121	VLPFSFAWPRSYTLLEAVEADSSNDTVPQDSIIKASHSGMINSPROWTLKQNTGVAHFE	180
FT	DOMAIN	525	561	EGF-like 8.	QY	121		180
FT	DOMAIN	574	627	EGF-like 9.	QY	121		180
FT	DOMAIN	629	665	EGF-like 10; calcium-binding (Potential).	QY	181	YQIRVTCDDYYGFGCNKFCRPRDDFFGHYACDQNGKTCMEGMWPECNRAICROGCSP	240
FT	DOMAIN	667	703	EGF-like 11; calcium-binding (Potential).	QY	181		240
FT	DOMAIN	705	741	EGF-like 12.	QY	181		240
FT	DOMAIN	744	780	EGF-like 13.	QY	241	KHGSKCLPGDCRCQYGMQGLYCDKCIHPHGCYVHGI CNEPMQCLCETNMGQOLCKDLNYC	300
FT	DOMAIN	782	818	EGF-like 14; calcium-binding (Potential).	QY	241		300
FT	CARBOHYD	820	856	EGF-like 15; calcium-binding (Potential).	QY	301	GHQPCPLNGGTCNTGPDYKQSCPEGYSGPNCIEAIAHACLSDPCHNRSGCKETSJGFEC	360
FT	CARBOHYD	143	143	N-linked (GlnAc. . .) (Potential).	QY	301		360
FT	CARBOHYD	217	217	N-linked (GlnAc. . .) (Potential).	QY	301		360
FT	CARBOHYD	382	382	N-linked (GlnAc. . .) (Potential).	QY	361	ECSPGWTGPTCSNTIDDCSPNNCSHGTCQDLVNGFKVCVPPQWTGKTCQLDANECEAKP	420
FT	CARBOHYD	559	559	N-linked (GlnAc. . .) (Potential).	QY	361		420
FT	CARBOHYD	745	745	N-linked (GlnAc. . .) (Potential).	QY	421	CYNAKSKNLIASYCDCLPGWNGQNDININDCLQCCQNDASCRDLVNGYRICIPGYA	480
FT	CARBOHYD	960	960	N-linked (GlnAc. . .) (Potential).	QY	421		480
FT	CARBOHYD	991	991	N-linked (GlnAc. . .) (Potential).	QY	481	GDHCERDIDECASNPLCLNGHCHQNEINRFQCLCPTGFSGNLCOLDIDYCEPNPQNGAQC	540
FT	CARBOHYD	1045	1045	N-linked (GlnAc. . .) (Potential).	QY	481		540
FT	CARBOHYD	1064	1064	N-linked (GlnAc. . .) (Potential).	QY	541	YNRASYFCCKPEDYEGKNCCHLKHCRTPPCVIDSCTVAMASNDTPEGVRYISSNVCG	600
FT	DISULFID	300	312	By similarity.	QY	541		600
FT	DISULFID	306	322	By similarity.	QY	601	PHGKCKSQSGKFTCDCKNGFTGTGTYCHENINDCESNRCNGTCDIGVNSYKICSDGWE	660
FT	DISULFID	324	333	By similarity.	QY	601		660
FT	DISULFID	340	351	By similarity.	QY	661	GHQPCPLNGGTCNTGPDYKQSCPEGYSGPNCIEAIAHACLSDPCHNRSGCKETSJGFEC	720
FT	DISULFID	345	360	By similarity.	QY	661		720
FT	DISULFID	362	371	By similarity.	QY	721	YDEGDAFKCMCPGWEGLTTCNIARNSSCLPNPCHNGGTCTVNGSDSFTVCKEGWEPICT	780
FT	DISULFID	378	389	By similarity.	QY	781	QNTNDCSPHPCVNSGTCVVDGDNWYRCCECAPGAGPDCRININECQSSPCAFGATCTVDEIN	840
FT	DISULFID	383	398	By similarity.	QY	781		840
FT	DISULFID	400	409	By similarity.	QY	841	GYRCVCPHSGAKCOEVSGRPCITMGSVIPDGAKWDDCNTCCCLNGRITACSKVWCGPR	900
FT	DISULFID	416	427	By similarity.	QY	841		900
FT	DISULFID	421	436	By similarity.	QY	901	PCLLKHGHECPNGQSCIPVLDDQCFVRCCTGAGECRSSSLQPVKTKTSDSYQDNCA	960
FT	DISULFID	438	447	By similarity.	QY	901		960
FT	DISULFID	454	464	By similarity.	QY	961	ITFTFNKEMWSPGLTTEHI CSELRLNLIKNVSAEYSIYIACBPSPSANNEIHVAISAED	1020
FT	DISULFID	458	473	By similarity.	QY	961		1020
FT	DISULFID	475	484	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	491	502	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	511	511	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	516	522	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	529	540	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	534	549	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	551	560	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	578	605	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	599	615	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	617	626	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	633	644	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	638	653	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	655	664	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	671	682	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	676	691	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	693	702	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	709	720	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	714	729	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	731	740	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	748	759	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	753	768	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	770	779	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	786	797	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	791	806	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	808	817	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	824	835	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	829	844	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
FT	DISULFID	846	855	By similarity.	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067
SQ	SEQUENCE	1219	AA; 134326 MW; 65D4CFC238A0E204	CRC64;	QY	1021	IRDDGNPIKEITDKIIDLVSKRDSGNSSLIAAVALVQRPLKNRTD	1067

Query Match 97.5%; Score 6089; DB 1; Length 1219;  
Best Local Similarity 96.8%; Pred. No. 0;  
Matches 1033; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

RESULT 4  
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AC Q9QXX0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Jagged-1 precursor (Jagged1).  
GN Name=Jagi;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN NUCLEOTIDE SEQUENCE, AND RECEPTOR INTERACTION.  
RP STRAIN=Swiss Webster / NIH;  
RX MEDLINE=20020271; PubMed=10551863; DOI=10.1074/jbc.274.46.32961;  
RA Shimizu K., Chiba S., Kumano K., Hosoya N., Takahashi T., Kanda Y.,  
Hamada Y., Yazaki Y., Hirai H.;  
RT "Mouse Jagged1 physically interacts with Notch2 and other Notch  
RT receptors: assessment by quantitative methods.";  
RL J. Biol. Chem. 274:32961-32969(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Boas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20025753; PubMed=10556292; DOI=10.1093/hmg/8.13.2443;  
RA Loomes K.M., Underkoffler L.A., Morabito J., Gottlieb S.,  
RA Piccoli D.A., Spinner N.B., Baldwin H.S., Oakley R.J.;  
RT "The expression of Jagged1 in the developing mammalian heart  
RT correlates with cardiovascular disease in Alagille syndrome.";  
RL Hum. Mol. Genet. 8:2443-2449(1999).  
CC -!- FUNCTION: Ligand for multiple Notch receptors and involved in the  
CC mediation of Notch signaling. May be involved in cell-fate  
CC decisions during hematopoiesis. Seems to be involved in early and  
CC late stages of mammalian cardiovascular development. Inhibits  
CC myoblast differentiation (By similarity). May regulate fibroblast  
CC growth factor-induced angiogenesis.  
CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 and NOTCH3.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Widely expressed in many tissues, with highest  
CC expression in brain, heart, muscle and thymus.  
CC -!- DEVELOPMENTAL STAGE: At 8.75-9.75 dpc expression was detected in  
CC structures that include those destined to contribute to the  
CC cardiovascular system of the adult heart. Expression was also  
CC detected in the mesencephalon and rhombencephalon.  
CC -!- DOMAIN: The DSL domain is indispensable and sufficient for binding  
CC to NOTCH2.  
CC -!- SIMILARITY: Contains 1 DSL domain.

CC -!- SIMILARITY: Contains 15 EGF-like domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AF171092; AAP15505.1; -; mRNA.  
DR EMBL; BC058675; AAH58675.1; -; mRNA.  
DR HSSP; P00740; IEDM.  
DR Ensembl; ENSMUSG00000027276; Mus musculus.  
DR MGI; MGI:1095416; Jag1.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005509; F:calcium ion binding; NAS.  
DR GO; GO:0008083; F:growth factor activity; ISS.  
DR GO; GO:0005112; F:Notch binding; IPI.  
DR GO; GO:0005198; F:structural molecule activity; ISS.  
DR GO; GO:0001525; P:angiogenesis; ISS.  
DR GO; GO:0001709; P:cell fate determination; ISS.  
DR GO; GO:0045446; P:endothelial cell differentiation; ISS.  
DR GO; GO:0030097; P:hemopoiesis; ISS.  
DR GO; GO:0020216; P:keratinocyte differentiation; ISS.  
DR GO; GO:0002011; P:morphogenesis of an epithelial sheet; IMP.  
DR GO; GO:0045445; P:myoblast differentiation; ISS.  
DR GO; GO:0045596; P:negative regulation of cell differentiation; IMP.  
DR GO; GO:0007399; P:neurogenesis; ISS.  
DR GO; GO:0007219; P:Notch signaling pathway; ISS.  
DR GO; GO:0045639; P:positive regulation of myeloid cell differe. .; IDA.  
DR GO; GO:0045747; P:positive regulation of Notch signaling pathway; IDA.  
DR GO; GO:0042127; P:regulation of cell proliferation; ISS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_s.  
DR InterPro; IPR001774; DSL.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca\_bd.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR011651; MNML.  
DR Pfam; PF01414; DSL; 1.  
DR Pfam; PF00008; EGF; 11.  
DR Pfam; PF07645; EGF\_CA; 1.  
DR Pfam; PF07657; MNML; 1.  
DR PRINTS; PR00010; EGFBL00D.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 10.  
DR PROSITE; PS1051; DSL; 1.  
DR PROSITE; PS00022; EGF\_1; 16.  
DR PROSITE; PS01186; EGF\_2; 12.  
DR PROSITE; PS50026; EGF\_3; 15.  
DR PROSITE; PS01187; EGF\_CA; 8.  
KW Calcium; Developmental protein; EGF-like domain; Glycoprotein;  
KW Notch signaling pathway; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 33  
FT CHAIN 34 1218 Jagged-1.  
FT TOPO\_DOM 34 1067 Extracellular (Potential).  
FT TRANSMEM 1068 1093 Potential.  
FT TOPO\_DOM 1094 1218 Cytoplasmic (Potential).  
FT DOMAIN 185 229 DSL.  
FT DOMAIN 230 266 EGF-like 1; atypical.  
FT DOMAIN 296 334 EGF-like 2.  
FT DOMAIN 336 372 EGF-like 3.  
FT DOMAIN 374 410 EGF-like 4; calcium-binding (Potential).  
FT DOMAIN 412 448 EGF-like 5; calcium-binding (Potential).  
FT DOMAIN 450 485 EGF-like 6; calcium-binding (Potential).  
FT DOMAIN 487 523 EGF-like 7; calcium-binding (Potential).  
FT DOMAIN 525 561 EGF-like 8.  
FT DOMAIN 574 627 EGF-like 9.  
FT DOMAIN 629 665 EGF-like 10; calcium-binding (Potential).  
FT DOMAIN 667 703 EGF-like 11; calcium-binding (Potential).  
FT DOMAIN 705 741 EGF-like 12.  
FT DOMAIN 744 780 EGF-like 13.  
FT DOMAIN 782 818 EGF-like 14; calcium-binding (Potential).  
FT DOMAIN 820 856 EGF-like 15; calcium-binding (Potential).  
FT DOMAIN 820 856

FT	CARBOHYD	143	143	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	217	217	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	382	382	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	559	559	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	745	745	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	960	960	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	991	991	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	1045	1045	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	1064	1064	N-linked (GlcNAc. . .)	(Potential).
FT	DISULFID	300	312	By similarity.	
FT	DISULFID	306	322	By similarity.	
FT	DISULFID	324	333	By similarity.	
FT	DISULFID	340	351	By similarity.	
FT	DISULFID	345	360	By similarity.	
FT	DISULFID	362	371	By similarity.	
FT	DISULFID	378	389	By similarity.	
FT	DISULFID	383	398	By similarity.	
FT	DISULFID	400	409	By similarity.	
FT	DISULFID	416	427	By similarity.	
FT	DISULFID	421	436	By similarity.	
FT	DISULFID	438	447	By similarity.	
FT	DISULFID	454	464	By similarity.	
FT	DISULFID	458	473	By similarity.	
FT	DISULFID	475	484	By similarity.	
FT	DISULFID	491	502	By similarity.	
FT	DISULFID	496	511	By similarity.	
FT	DISULFID	513	522	By similarity.	
FT	DISULFID	529	540	By similarity.	
FT	DISULFID	534	549	By similarity.	
FT	DISULFID	551	560	By similarity.	
FT	DISULFID	578	605	By similarity.	
FT	DISULFID	599	615	By similarity.	
FT	DISULFID	617	626	By similarity.	
FT	DISULFID	633	644	By similarity.	
FT	DISULFID	638	653	By similarity.	
FT	DISULFID	655	664	By similarity.	
FT	DISULFID	671	682	By similarity.	
FT	DISULFID	676	691	By similarity.	
FT	DISULFID	693	702	By similarity.	
FT	DISULFID	709	720	By similarity.	
FT	DISULFID	714	729	By similarity.	
FT	DISULFID	731	740	By similarity.	
FT	DISULFID	748	759	By similarity.	
FT	DISULFID	753	768	By similarity.	
FT	DISULFID	770	779	By similarity.	
FT	DISULFID	786	797	By similarity.	
FT	DISULFID	791	806	By similarity.	
FT	DISULFID	808	817	By similarity.	
FT	DISULFID	824	835	By similarity.	
FT	DISULFID	829	844	By similarity.	
FT	DISULFID	846	855	By similarity.	
SQ	SEQUENCE	1218 AA; 134164 MW; 77739F8928BB793C CRC64;			
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Best Local Similarity 96.8%; Pred. No. 0;					
Matches 1033; Conservative 15; Mismatches 19; Indels 0; Gaps 0;					
QY	1	MRSPRTGRSGRPLSLALLCALRAKVCASGQFLEILSMQNVGELQNGCCGARN	60		
Db	1	MRSPRTGRSGRPLSLALLCALRAKVCASGQFLEILSMQNVGELQNGCCGVRN	60		
QY	61	PGDRKCTRDECDTYFKVCLKEYQSRVTAGPCSPGSGSTPVGNTFNLKASRGNDRNI	120		
Db	61	PGDRKCTRDECDTYFKVCLKEYQSRVTAGPCSPGSGSTPVGNTFNLKASRGNDRNI	120		
QY	121	VLPSFAWPSRYTLLVEAWDSNDTVPDSIIIEKASHSGMINPSROWTLKQNTGVAHFE	180		
Db	121	VLPSFAWPSRYTLLVEAWDSNDTIQDIIIEKASHSGMINPSROWTLKQNTGIAHFE	180		
QY	181	YQIRVTCDDYYFGGNKFCRPRDDPFHGYACDQNGKTCMEGWMPGCNRAICROGCSP	240		
Db	181	YQIRVTCDDHYFGGNKFCRPRDDPFHGYACDQNGKTCMEGWMPGCNKAI CROGCSP	240		

Qy	241	KHGSCKLPBDCRCQYQWGLYCDKCIHPQCIVHGI	CNEPWCICETNWGSQLCDKOLNYC	300
Db	241	KHGSCKLPBDCRCQYQWGLYCDKCIHPQCIVHGI	CNEPWCICETNWGSQLCDKOLNYC	300
Qy	301	GTHQPCNLNGGTCSNTGPDKYQCSCEPGYSGPNCIEA	HACLSDPCHNRGSKCTSLGPEC	360
Db	301	GTHQPCNLNGGTCSNTGPDKYQCSCEPGYSGPNCIEA	HACLSDPCHNRGSKCTSLGPEC	360
Qy	361	ECSFGWTGPTCTSTNIDDCSPNNCSHGTCQDLVNGFK	VCVPPQWTKTCTOLDANECEAKP	420
Db	361	ECSFGWTGPTCTSTNIDDCSPNNCSHGTCQDLVNGFK	VCVPPQWTKTCTOLDANECEAKP	420
Qy	421	CYNAKSKNLIASYCDCLPGWNGQCDININCLGQCDND	ASCRDLVNGYRCICPPGYA	480
Db	421	CYNAKSKNLIASYCDCLPGWNGQCDININCLGQCDND	ASCRDLVNGYRCICPPGYA	480
Qy	481	GDHCERDIDECASNPLCNGHGHCHQNEINRFOLCPT	FTGFSGNLCOLDIDYCEPNPQNGAQC	540
Db	481	GDHCERDIDECASNPLCNGHGHCHQNEINRFOLCPT	FTGFSGNLCOLDIDYCEPNPQNGAQC	540
Qy	541	YNRASDYFKCPCPEDEYEGKNCSHLKHCRTRTPCE	VIDSCTVMAASNDTPEGVRYISSNVCG	600
Db	541	YNRASDYFKCPCPEDEYEGKNCSHLKHCRTRTPCE	VIDSCTVMAASNDTPEGVRYISSNVCG	600
Qy	601	PHGCKSQSGGKFTCDCKNGFTGTYCHENINDCESNP	CRNGGTCIDGVNSYKICISDGWE	660
Db	601	PHGCKSQSGGKFTCDCKNGFTGTYCHENINDCESNP	CRNGGTCIDGVNSYKICISDGWE	660
Qy	661	GAYCETINDCSONPCHNGGTCRDLVNDFYCDCKNG	WKGTCHSRDSQCDCEATCNGGTC	720
Db	661	GAYCETINDCSONPCHNGGTCRDLVNDFYCDCKNG	WKGTCHSRDSQCDCEATCNGGTC	720
Qy	721	YDEGDAFKMCPGGWEGTTCNIARNSSCLPNPCHNG	GTCTVYNGESFTCVCKEGWEGPICA	780
Db	721	YDEGDAFKMCPGGWEGTTCNIARNSSCLPNPCHNG	GTCTVYNGESFTCVCKEGWEGPICA	780
Qy	781	QNTNDCSPHPCYNSGTCVDGDNWYRCCECAPAGP	DCRININECQSSPCAFGATCVDEN	840
Db	781	QNTNDCSPHPCYNSGTCVDGDNWYRCCECAPAGP	DCRININECQSSPCAFGATCVDEN	840
Qy	841	GYRCVCPGHSGAKCOEVSGRPCITWGSVTPDCAK	WDDCNTCQCLNGRACSKVWCGR	900
Db	841	GYRCVCPGHSGAKCOEVSGRPCITWGSVTPDCAK	WDDCNTCQCLNGRACSKVWCGR	900
Qy	901	PCLLHGHSECPSSQSCIPILDDQCFVHPCTGVGEC	RSSSLQPVTKTCTSDSYQDNCAN	960
Db	901	PCLLHGHSECPSSQSCIPILDDQCFVHPCTGVGEC	RSSSLQPVTKTCTSDSYQDNCAN	960
Qy	961	ITPTFNKEMWSPGLTTEHICSELURNILKNVSAEY	SIYIACPPSPSANNHVAISAED	1020
Db	961	ITPTFNKEMWSPGLTTEHICSELURNILKNVSAEY	SIYIACPPSPSANNHVAISAED	1020
Qy	1021	IRDDGNPIKETDKIIDLVSKRDNSSLIATAVAEVR	QRRPLKNRTD 1067	
Db	1021	IRDDGNPIKETDKIIDLVSKRDNSSLIATAVAEVR	QRRPLKNRTD 1067	
RESULT 5				
Q90819 CHICK				
ID	Q90819	CHICK PRELIMINARY;	PRT; 1193 AA.	
AC	Q90819			
DT	01-NOV-1996	(TrEMBLrel. 01, Created)		
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)		
DE	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	C-Serate-1	protein (Fragment).		
OS	Gallus gallus	(Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata;	Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes;	Phasianidae; Phasianinae;		
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Otic explant, and Spinal cord;			



```
RX MEDLINE=96175595; PubMed=8631496; DOI=10.1006/dbio.1996.0069;
RA Myat A., Henrique D., Ish-Horowicz D., Lewis J.;
RT "A chick homologue of Serrate and its relationship with Notch and
RL Delta homologues during central neurogenesis.";
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR ENBL; X95283; CAA64604.1; -; mRNA.
DR HSP; P00740; IEDM.
DR Ensembl; ENSGALG00000009020; Gallus gallus.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005509; F: calcium ion binding; IEA.
DR GO; GO:0007154; P: cell communication; IEA.
DR GO; GO:0007275; P: development; IEA.
DR GO; GO:0007219; P: Notch signaling pathway; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011651; MNLL.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 12.
DR Pfam; PF07645; EGF_Ca; 1.
DR Pfam; PF07657; MNLL; 1.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PSS1051; DSL; 1.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS00026; EGF_3; 16.
DR PROSITE; PS01187; EGF_CA; 8.
KW Developmental protein; EGF-like domain; Notch signaling pathway.
FT NON_TER 1
SQ SEQUENCE 1193 AA; 131040 MW; 24E94D09B987935 CRC64;

Query Match 87.5%; Score 5469.5; DB 2; Length 1193;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 907; Conservative 57; Mismatches 77; Indels 1; Gaps 1;

Qy 27 KVGASGQFELEILSMQVNGELQNGCCGARNPGDKCTRDCEDTYFKVCLKEYQSRV 86
Db 1 QVASASGQFELEILSVQVNGVLQNGCCDGRNPGDKCTRDCEDTYFKVCLKEYQSRV 60

Qy 87 TAGGFCFGSGSTPVIQNTFNLKASRGDNRIVLPSFAWPRSYTLVVEAWDSSNDTV 146
Db 61 TAGGFCFGSGSTPVIQNTFNLKYSRNEKNRIVIPFSAWPRSYTLVVEAWDYNNDST 120

Qy 147 QPDSIIKASHSGMINPSRQWTLKQNTGVAFHYQIRVTCDDYYGYFGCNKFCRPRDDF 206
Db 121 NPDRIIKASHSGMINPSRQWTLKHTGAHFIYQIRVTCAEHYGYFGCNKFCRPRDDF 180

Qy 207 FGHYACDQNGKTCMEGWMGPECNRAICRQCSFKHGSCKLPGDCRCQYGNQGLYCKICI 266
Db 181 FTHHTCDQNGKTCLEGTGPECNKAICRQCSFKHGSCTVPGECCRCQYGNQGLYCKICI 240

Qy 267 PHPCGVHGI CNEPQCLCETNWGQLCDKLDNYCGTHQPCCLNGCTCSNTPGDKYQCSCE 326
Db 241 PHPCGVHGTCTEPWQCLCETNWGQLCDKLDNYCGTHPPCLNGCTCSNTPGDKYQCSCE 300

Qy 327 GYSFPNCIEAHACLSDPCNHRGSKETSLGFCECSPGWTGPTCSNIDDCSPNNCSHG 386
Db 301 GYSQNCIEAHACLSDPCNHRGSKETSLGFCECSPGWTGPTCSNIDDCSPNNCSHG 360

Qy 387 GTCQDLVNGFKVCPQWTKTQCLDANECEBAKPCVNAKSKNLIASVYCDCLPGWQGN 446
Db 361 GTCQDLVNGFKVCPQWTKTQCLDANECEBAKPCVNAKSKNLIASVYCDCLPGWQGN 420
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DR InterPro; IPR001774; DSL..
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR011651; MNFL.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 13.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF07657; MNFL; 1.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PSS0026; EGF_3; 15.
DR PROSITE; PS01187; EGF_CA; 8.
DR PROSITE; PS01187; EGF_CA; 8.
SQ SEQUENCE 1214 AA; 133807 MW; A9C09C420CC157C2 CRC64;

Query Match 84.2%; Score 5263; DB 2; Length 1214;
Best Local Similarity 82.3%; Pred. No. 0;
Matches 879; Conservative 87; Mismatches 96; Indels 6; Gaps 4;

QY 1 MRSPTGRSGRPLSLALLCALRAKVCAGSGQFELEILSMQNVGELQNGCCGGAN 60
DB 1 MRFPRL--RALSPL-LVSALLLRLIKVSIASGQFELEILSMQNPGLQSGNCCDQRN 56

QY 61 PGRKCTRDRCDFYFKVCLKEYQSRVTAGPCSPGSGSTVPIGNTNFKASGRNDR 120
DB 57 PDRKCRDRCDYFYFKVCLKEYQSRVSAGGACSFGTGYTPIVIGNSFNLYSRNERN 116

QY 121 VLPFSFAPWSYTLLEAVDSSNDTQVDSIIKASHGMINSPROWOTLKONTGVVAF 180
DB 117 VLPFSFAPWSYTLLEAVDSSNDTQVDSIIKASHGMINSPROWOTLKONTGVVAF 176

QY 181 YQIRVTCDYYFGCNKFCRPRDDFFGHYACDQNGKTCMEGMGPECNRAICRQCS 240
DB 177 YQIRVICDEHYFGCNKFCRPRDDFFGHYTCDLNGNKTCLGWMGPECSTAI 236

QY 241 KHGSKLPGRCRCQYHGOGLYCDKIPHPGCVHGI CNEPWCICETWGGQLCDK 300
DB 237 KHGCTKTPGRCRCQYHGOGLYCDKIPHPGCVHGT CNEPWCICETWGGQLCD 296

QY 301 GTHPQCLNGTCSNTGPDKYQCSPEGYSGPNCBIAEHAACLSDPCHNRGSKETS 360
DB 297 GTYQPCNLNGTCSNTGPDKYQCSPEGYSGQNCBIAEHAACLSDPCHNGGSL 356

QY 361 ECSFGWTGPTCSTNIDPCSPNCSHGTCQDLVNGFKVCVCPQWTKTKCOLDANE 420
DB 357 QCARGWTGPTCSINIDCSFNPCGYGTCQDLIDGFKVICPSQWTKTKCOLDANE 416

QY 421 CVNAKSKNLIASYCDCLPGWQNGCDININDCLGQONDASCRDLVNGYRCICPP 480
DB 417 CVNANSRNLIGSYCNCLPGWQNGCDININDCLGQONGTCKDLVNGYRCICPP 476

QY 481 GDHCERDIDRCANPCLNGHGCNEINRFQCLPTGFSGNLCOLDIDYCEPNPCON 540
DB 477 GBCEKDVNCEVSNPCLNGHGCNEINRFQCLPTGFSGNLCOLDIDYCEPNPCON 536

QY 541 YNRASDYFKCPEDYEGKNCNHLKDHCRTPPCVIDSDCTVAMASNDTPPEGV 600
DB 537 FNLATDYFCNSEDYEGKNCNHLKDHCRTPPCVIDSDCTVAMASNDTPPEGV 596

QY 601 PHGKCSQSGKFTCDCKNGFTGTGYCHENINDCESNPCRNGGTCDIGVNSYKIC 660
DB 597 PHGKCSQSGKFTCECKNGFTGTGYCHENINDCESNPCRNGGTCDIGVNSYKIC 656

QY 661 GAYCETNINDCONPCHNGTCDRLVNDYFCDCKNGWKGTCHSRQSCDEATCN 720
DB 657 GYICETNINDCONPCHNGTCDRLVNDYFCECKNGWKGTCHSRQSCDEATCN 716
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RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084953.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Aax_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR011651; MNML.
DR InterPro; IPR006552; VWC out.
DR InterPro; IPR001007; VWF-C.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 13.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF07657; MNML; 1.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 16.
DR SMART; SM00179; EGF_CA; 14.
DR SMART; SM00214; VWC; 1.
DR SMART; SM00215; VWC out; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 16.
DR PROSITE; PS01185; EGF_2; 12.
DR PROSITE; PS00026; EGF_3; 15.
DR PROSITE; PS01187; EGF_CA; 8.
SQ SEQUENCE 1051 AA; 114851 MW; 519BCA8DD3786222 CRC64;

Query Match      83.6%; Score 5225; DB 2; Length 1051;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 871; Conservative 86; Mismatches 93; Indels 6; Gaps 4;

Qy 1 MRSPTRGSRPLSLALLCALRAKVCAGSGQFELEILSMQNVNGLQNGMCCGARN 60
Db 1 MRPPR---RALSP-LVSAALLCLRKIVSIASGQFELEILFMQNPNGELQSGNCCDQGN 56

Qy 61 PGRKCTRDCTDYFKVCLKEYQSRVTAGGPGSGSTVPIGGTNTNLKASRGNDRNI 120
Db 57 PTDRKCRDECDTYFKVCLKEYQSRVSAGGACSGFTGYTPVIGGNSFNLYSRNNERNRI 116

Qy 121 VLPSFAWPRSYTLVLEAWDSNDTVPDSIIKASHSGMINPFRQWOTLKQNTGVVAFH 180
Db 117 VLPSFAWPRSYTLVLEAWDYNNDTDPGLDIDKALHSGMINPFRQWOTLKQNGMTYFE 176

Qy 181 YQIRVTCDDYYVFGCNKFCRPRDDFFGHYACDQNGKNTCMEGWMPFNCRNACRQCSP 240
Db 177 YQIRVTCDDYYVFGCNKFCRPRDDFFGHYTCDLNGKNTCLEGWMPFECSTAI CRQCSS 236

Qy 241 KHGSKLPDCRCQYGHQGLYCDKICIPHPGCVHGI CNEPWQCLCTETWGGQLCKDILNYC 300
Db 237 KHGCTKTPGECRCQYGHQGLYCDKICIPHPGCVHGT CNEPWQCLCTETWGGQLCKDILNYC 296

Qy 301 GTHQPLNGGTCSTNIDPDKYQCSPEGYSGNCRCEIAHACLSDDPCHNGSGCLETSLGFEC 360
Db 297 GTYQPLNGGTCSTNIDPDKYQCSPEGYSGNCRCEIAHACLSDDPCHNGSGCLETSLGFEC 356

Qy 361 ECSPGWTGPTCTSTNIDPSPNCSHGFTCDLVNPGKVCVCPQWTKTQCDLANECCRAKP 420
Db 357 QCARGWTGPTCSINIDPSPNCPGCVGGTCDLIDFGFKICPSQWTKTQCDLANECCRAKP 416

Qy 421 CVNAKSKNLTASYCDCLPCWNGQNCNDINIDCLGQCONDASCRDLVNGVRCICPGYA 480
Db 417 CVNANSCRNLGYSYCNCLPGWTKQNCNDINIDCLGQCONDASCRDLVNGVRCICPGYA 476

Qy 481 GDHCERDIDECASNPLNGGHCQNEINRFOCLCTPTGSGNLQCLDIDYCEPNPQNGAQ 540

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Db 477 GERCEKDVNECVSNPCLNGSHGQDEINGFOCLCPAGFSGNLQCLDIDYCEPDPQNGAQ 536
Qy 541 YNPASDYFKCPEDYEGKNCCHLKHCRTPTPCEVIDSCTVAMASNDTPPEGVRISSNVCG 600
Db 537 FNLATDYFCNSEDYEGKNCCHLKHCRTPTPCEVIDSCTVAMASNDTPPEGVRISSNVCG 596
Qy 601 PHGKCKSQSGGKFTCDNKGFTGTGTYCHENINDCESNPRNGGTCTIDGVNSYKICSDGWE 660
Db 597 PHGKCKSQSGGKFTCECKGFTGTGTYCHENINDCESNPRNGGTCTIDGVNSYKICSDGWE 656
Qy 661 GAYCETNINDCSQNPCHNGGTCDLVNDFYCDCKNGKMGKTCCHSRDSQCDDEATCNGGTC 720
Db 657 GIYCETNINDCSKNPCVNGGTCDLVNDFYCECKNGKMGKTCCHSRDSQCDDEATCNGGTC 716
Qy 721 YDEGDAPKCMCPGWEWGTTCNIARNSSCLPNPCHNGGTCTVVGESFTCVCKEGWEGPICA 780
Db 717 YDEGDTFKCICSPWEGATCNIARNSSCLPNPCHNGGTCTVVGESFTCVCKEGWEGTCS 776
Qy 781 QNTNDCSPHPCVNSGTCTVDGDNWYRCCECAPGAGPDCRININECQSSPCAFGATCVDEIN 840
Db 777 QNTNDCSPHPCVNSGTCTVDGDNWYRCCECAPGAGPDCRININECQSSPCAFGATCIDEIN 836
Qy 841 GYRCVCPGHSAGKCOEVSGRPCITMGSVIPDGAkWDDCNTCCLNGRIACSKVWCGPR 900
Db 837 GYRCCTCPGRSGPRCQEVTPGRPCITNGHMPDGEKWNDDCNSCQCLNGKVTCSKVWCGPQ 896
Qy 901 PCLLHKGHSECPGSGQSCIPILDDQCFVHPTCTGTCGECSSSLQPVKTKTSDSYQD-NCA 959
Db 897 RCDIN-GDSECPAGQTCVPRDNDHCFVPTCTGTCGECWPTNPQVTKCNANASYQDASCA 955
Qy 960 NITFTFNKEMMSPLTTEHICSELNINILKNVSAEYSIYIACEPSPSANNEIHVAISAE 1019
Db 956 NITFTFNKEMMSPLTTEHICSELNINILKNVSAEYSIYIACEPSPSANNEIHVAISAE 1015
Qy 1020 DIRDDGNPIKEITDKIIDLVSKRDGNSSLIAAFAEV 1055
Db 1016 ENGDRNPVKDITERIIDLVSKRDANNTFIASVAEV 1051

RESULT 8
JAG1B BRARE STANDARD; PRT; 1213 AA.
AC Q90Y54;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Jagged-1b precursor (Jagged1b) (Jagged3).
GN Name=jag1b; Synonyms=jag3;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oda T., Chandrasekharappa S.C.;
RT "Isolation, characterization and expression analysis of zebrafish
  Jagged genes.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ligand for Notch receptors and involved in the mediation
  of Notch signaling (By similarity). Seems to be involved in cell-
  fate decisions.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -!- SIMILARITY: Contains 17 EGF-like domains.
CC -!- SIMILARITY: Contains 1 VWF domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.

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	EMBL; AF229451; AAL08216.1; -, mRNA.	
CC	HSP; Q12780; IHR.	
DR	ZFIN; ZDB-GENE-011128-4; jaglb.	
DR	GO; GO:0001889; P:liver development; IGI.	
DR	InterPro; IPR000152; Asx_hydroxyl_S.	
DR	InterPro; IPR001774; DSL.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca_bd.	
DR	InterPro; IPR001438; EGF II.	
DR	InterPro; IPR006209; EGF-like.	
DR	InterPro; IPR011651; MNNE.	
DR	InterPro; IPR01007; VWF_C.	
DR	Pfam; PF00444; DSL; 1.	
DR	Pfam; PF00008; EGF; 12.	
DR	Pfam; PF07645; EGF CA; 1.	
DR	Pfam; PF07657; MNNE; 1.	
DR	PRINTS; PR00010; EGFBLD.	
DR	SMART; SM00051; DSL; 1.	
DR	SMART; SM00179; EGF_CA; 10.	
DR	SMART; SM00214; VMC; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 10.	
DR	PROSITE; PS1051; DSL; 1.	
DR	PROSITE; PS00022; EGF_1; 16.	
DR	PROSITE; PS01186; EGF_2; 12.	
DR	PROSITE; PS00026; EGF_3; 15.	
DR	PROSITE; PS01187; EGF CA; 8.	
DR	PROSITE; PS01208; VWF_C; FALSE NEG.	
DR	PROSITE; PS01208; VWF_C; FALSE NEG.	
KW	Calcium; Developmental_protein; EGF-like domain; Glycoprotein;	
KW	Notch signaling pathway; Repeat; Signal; Transmembrane.	
FT	SIGNAL 1 26 Potential.	
FT	CHAIN 27 1213 Jagged-1b.	
FT	TOPO_DOM 27 1064 Extracellular (Potential).	
FT	TRANSEM 1065 1087 Potential.	
FT	TOPO_DOM 1088 1213 Cytoplasmic (Potential).	
FT	DOMAIN 182 226 DSL.	
FT	DOMAIN 227 260 EGF-like 1.	
FT	DOMAIN 258 291 EGF-like 2.	
FT	DOMAIN 293 331 EGF-like 3.	
FT	DOMAIN 333 369 EGF-like 4.	
FT	DOMAIN 371 407 EGF-like 5; calcium-binding (Potential).	
FT	DOMAIN 409 445 EGF-like 6; calcium-binding (Potential).	
FT	DOMAIN 447 482 EGF-like 7; calcium-binding (Potential).	
FT	DOMAIN 484 520 EGF-like 8; calcium-binding (Potential).	
FT	DOMAIN 522 558 EGF-like 9.	
FT	DOMAIN 592 624 EGF-like 10.	
FT	DOMAIN 626 662 EGF-like 11; calcium-binding (Potential).	
FT	DOMAIN 664 700 EGF-like 12; calcium-binding (Potential).	
FT	DOMAIN 702 738 EGF-like 13.	
FT	DOMAIN 746 777 EGF-like 14.	
FT	DOMAIN 779 815 EGF-like 15; calcium-binding (Potential).	
FT	DOMAIN 817 853 EGF-like 16; calcium-binding (Potential).	
FT	DOMAIN 860 914 VMC.	
FT	DOMAIN 918 956 EGF-like 17.	
FT	COMPAS 938 941 Poly-Pro.	
FT	CARBOHYD 139 139 N-linked (GlcNAc..) (Potential).	
FT	CARBOHYD 214 214 N-linked (GlcNAc..) (Potential).	
FT	CARBOHYD 556 556 N-linked (GlcNAc..) (Potential).	
FT	CARBOHYD 742 742 N-linked (GlcNAc..) (Potential).	
FT	CARBOHYD 957 957 N-linked (GlcNAc..) (Potential).	
FT	CARBOHYD 988 988 N-linked (GlcNAc..) (Potential).	
FT	CARBOHYD 1042 1042 N-linked (GlcNAc..) (Potential).	
FT	DISULFID 231 242 By similarity.	
FT	DISULFID 235 248 By similarity.	
FT	DISULFID 250 259 By similarity.	
FT	DISULFID 262 273 By similarity.	
FT	DISULFID 268 279 By similarity.	
FT	DISULFID 281 290 By similarity.	
FT	DISULFID 297 309 By similarity.	
FT	DISULFID 303 319 By similarity.	
FT	DISULFID 321 330 By similarity.	
FT	DISULFID 337 348 By similarity.	

Qy	556	EGKNCSLKDHCRTPCEVIDSDCTVAMASNDTPEGVYIISNVCGPHGKCKSOSGGKFTC	615	DR	ZFIN; ZDB-GENE-011128-2; jagla.
Db	553	EGKNCSLKDHCRTPCEVIDSDCTVAMASNDTPEGVYIISNVCGPHGKCKSOSGGQFTC	612	DR	InterPro; IPR000152; Asx_hydroxyl_s.
Qy	616	DCNKGFTGTCHENINDCESNCRNGTCTIDGVNSKYKICSDGWEAGYCACTNINDCSQNP	675	DR	InterPro; IPR0001774; DSL
Db	613	ECQEGFGTGTCHENINDCESNCRNGTCTIDGVNSKYKICSDGWEAGYCACTNINDCSQNP	672	DR	InterPro; IPR000742; EGF_2.
Qy	676	CHNGGTCDLVNDPYCDKNGWKTKCHSRSDSCDEATCNNGGTCYVDGAFKCMCPGGW	735	DR	InterPro; IPR001881; EGF_Ca_bd.
Db	673	CLNKGACQDLVNDPYCDKNGWKTKCHSRSDSCDEATCNNGGTCYVDGAFKCMCPGGW	732	DR	InterPro; IPR001438; EGF_II.
Qy	736	EGTTCNTARNSCLPNCHNGTCTVNGESFTCVCKEGWEGPICAQNTNDCSHPCCVNSG	795	DR	InterPro; IPR006209; EGF_like.
Db	733	EGATCNTAKNSCLPNCHNGTCTVNGESFTCVCKEGWEGPICAQNTNDCSHPCCVNSG	792	DR	InterPro; IPR011651; MNNL.
Qy	796	TCVDGDNWYCECAPGAGPDCRININECOSSPCAFATCVDINGYRCVCPGPHSGAKC	855	DR	InterPro; IPR001007; VWF_C.
Db	793	TCVDGDNWYCECAPGAGPDCRININECOSSPCAFATCVDINGYRCVCPGPHSGAKC	852	DR	Pfam; PF00008; EGF_13.
Qy	856	QEVSGRPCITWGSVIPDGAQWDDCNTCQCLNGRIACSKVWCGRPRCLLHKHSECPSPGQ	915	DR	PRINTS; PR00010; EGFBL00D.
Db	853	QEVVGRPCIANQVTDAGAKWEEDCNTCQCGRIHCTMWCGRPKSCRIGKARGGCPASQ	912	DR	SMART; SM00051; DSL; 1.
Qy	916	SCPIILDQCFVHCTGVGCRSSLOPVKTKC-TSDSYVDNCANITFTFNKEMKSPGL	974	DR	SMART; SM00179; EGF_CA; 9.
Db	913	SCVPIKEQCFVHCTGVGCRSSLOPVKTKC-TSDSYVDNCANITFTFNKEMKSPGL	971	DR	SMART; SM00214; VWC; 1.
Qy	975	TTEHCSELNLTNLTKNVSAEYSIYIACEPSPSANNHVAISAEIRDGNPKETDK	1034	DR	PROSITE; PS00010; ASX_HYDROXYL; 9.
Db	972	SVEHVCNELRHWWLLKNLTSTAYVSIACEPSSASNEIHISISTEERTDRSPKIDITVQ	1031	DR	PROSITE; PS1051; DSL; 1.
Qy	1035	IIDLVSXKRGDSSIIAAVAVRVRRLKNTD 1067		DR	PROSITE; PS00022; EGF_1; 16.
Db	1032	IIDLVSXKRGDSSIIAAVAVRVRRLKNTD 1063		DR	PROSITE; PS01186; EGF_2; 12.
RESULT 9					PROSITE; PS00026; EGF_3; 15.
AD	JAGIA_BRARE	STANDARD;	PRT; 1242 AA.	FT	PROSITE; PS01187; EGF_CA; 8.
ID	JAGIA_BRARE	STANDARD;	PRT; 1242 AA.	KW	Calcium; Developmental protein; EGF-like domain; Glycoprotein;
AC	Q90Y57;			KW	Notch signaling pathway; Repeat; Signal; Transmembrane.
DT	28-FEB-2003 (Rel. 41, Created)			FT	POTENTIAL
DT	28-FEB-2003 (Rel. 41, Last sequence update)			FT	CHAIN 29 1242
DT	13-SEP-2005 (Rel. 48, Last annotation update)			FT	TOPO_DOM 29 1070
DE	Jagged-1a precursor (Jagged1a) (Jagged1).			FT	TRANSMEM 1071 1095
GN	Name=Jagla; Synonyms=jagl;			FT	TOPO_DOM 1096 1242
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			FT	DOMAIN 186 230
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			FT	DOMAIN 231 264
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			FT	DOMAIN 262 295
OC	Cyprinidae; Danio.			FT	DOMAIN 297 335
OX	NCBI_TaxID=7955;			FT	DOMAIN 337 373
RP	(1)			FT	DOMAIN 375 411
RP	NUCLEOTIDE SEQUENCE.			FT	DOMAIN 413 449
PA	Oda T.; Chandrasekharappa S.C.;			FT	DOMAIN 451 486
RT	"Isolation, characterization and expression analysis of zebrafish			FT	DOMAIN 488 524
RT	Jagged genes."			FT	DOMAIN 526 562
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			FT	DOMAIN 575 630
CC	-1- FUNCTION: Ligand for multiple Notch receptors and involved in the			FT	DOMAIN 632 668
CC	mediation of Notch signaling (By similarity). Seems to be involved			FT	DOMAIN 670 706
CC	in cell-fate decisions.			FT	DOMAIN 708 744
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			FT	DOMAIN 747 783
CC	-1- SIMILARITY: Contains 1 DSL domain.			FT	DOMAIN 785 821
CC	-1- SIMILARITY: Contains 17 EGF-like domains.			FT	DOMAIN 823 859
CC	-----			FT	DOMAIN 859 959
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			FT	DOMAIN 959 991
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			FT	DOMAIN 991 991
CC	the European Bioinformatics Institute. There are no restrictions on its			FT	DOMAIN 1046 1046
CC	use as long as its content is in no way modified and this statement is not			FT	DOMAIN 1046 1046
CC	removed.			FT	DOMAIN 1046 1046
CC	-----			FT	DOMAIN 1046 1046
DR	EMBL; AF229448; AAL08213.1; -; mRNA.			FT	DOMAIN 1046 1046
DR	HSP; P01132; 1GK5.			FT	DOMAIN 1046 1046

FT	DISULFID	455	465	By similarity.	603	GKCKSQS--GGKFTCDNKGFTGTCTYCHENINDCESNPRNGGTCIDGVNSYKICISDGWE	660
FT	DISULFID	459	474	By similarity.	604	GRCRSHAGGHPSCDQDQDFTGTCTYCHENINDCESSCLSGGTICDKINAYQCICADGWE	663
FT	DISULFID	476	485	By similarity.	661	GAYCETININDSONPCHNGGTCRDLYNDFYCDCKNGMKGTCHSRDSQCDATCNGGTC	720
FT	DISULFID	492	503	By similarity.	664	GPNCETINIDCRTNPCRDRGVCRDLVNDFYCECENGWKGKTCCHSRQSCDDETCNNGGTC	723
FT	DISULFID	497	512	By similarity.	721	YDEGDAPKCMCPGWEGETTCNTIARNSSCLPNPCHNGGTCVYNGESFTCVCKEGWEGPICA	780
FT	DISULFID	514	523	By similarity.	724	SDEGDSFKCLCSPGWEGATCNIAKNSSCLPNPCENGATCVVTDGFTCVCKEGWEGPICS	783
FT	DISULFID	523	541	By similarity.	781	QNTNDCSPHCYNSTGTCVGDNDWYRCCECAPGAPGPRININECQSSPCAFGATCVDDEIN	840
FT	DISULFID	530	541	By similarity.	784	QNSNDCNPQPCYNSTGTCVGDNDWYRCCECAPGAPGPRININECQSSPCAFGATCVDDEIN	843
FT	DISULFID	535	550	By similarity.	841	GYRCVCPPHSGAKCOEVSGRPCITMGSVIPDCAKWDCCNTCCQCLNGRTACSKVWCGPR	900
FT	DISULFID	552	561	By similarity.	844	GYRCLCPGRTGPRCOEVTGRCVIGRTAVDGAQKWAEDCNTCYCHKGIVTCTKLCGPK	903
FT	DISULFID	561	571	By similarity.	901	PC-LLHKGHSBCPSGQSCIPILDQCFVHPCTGTVGECRSSSLQPVTKTCTSDSYQDNCA	959
FT	DISULFID	566	577	By similarity.	904	ACRMLGSGRGDCPTGQLCVPRDEQCFVKPCSSQGCWSAHRPAVRTHCQPDSSH---CA	959
FT	DISULFID	572	582	By similarity.	960	NTFTFNKEMSPGLTTEHCSELNMLNKLNVASYSYIACIPEPSANNEIHVAISAE	1019
FT	DISULFID	573	583	By similarity.	960	NVTFTFNKDTMPQGVTVQVCRHLRYTKNTVSFISVSCELSSAASNEIHVAHVT	1019
FT	DISULFID	574	584	By similarity.	1020	DIRDDGN-PIKETDKIIDLVSKRDNSSIIAIAVAEVRVQRRLKN	1064
FT	DISULFID	575	585	By similarity.	1020	ENGIHRVPVKEITDNIIDLVSKHSANSSVIGSIAEVRVQRKQPN	1065
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FT	DISULFID	772	782	By similarity.			
FT	DISULFID	773	783	By similarity.			
FT	DISULFID	7					





Matches	655;	Conservative	137;	Mismatches	239;	Indels	18;	Gaps	8
Qy	27	KVCGASGQFELIILSMQNVGELQNGCCGARNPGDKTRDECDTYFKVCKLEYOSRV	86						
Db	1	QVSRGTGVFELQNLNSVRNVGELLNGECCDGERNPDPDRDCGRDECDTVVKVCKLEYQAKI	60						
Qy	87	TAGGPCSPGSGSTPVIIGGNTFNLKA-----SRGNDNRNRIVLPSFPAPRPSRYTILLVEAWD	140						
Db	61	SPGPGCSYSGSGSTPVLGGNLIYLANGDKYHPHGRSPETGRIVIPFYQAWPRSFYLLILEAWD	120						
Qy	141	SSNDTVQ--PDGIIIEKASHSGMINPSROWTLKONTGVAHFVQIRVTCDDYVYGFGCNKF	199						
Db	121	WDNUTKSGEDLLIERVAHAGMINPEDRWKTLOFGVPANFEVQIRVKCDENYIYALCNKF	180						
Qy	200	CRPRDDPFHYACDQNGNKTCMEGMMGPECNRAICROGCSPKHGSCKLPGDCRCQYGMQG	259						
Db	181	CGPRDDFVGHVTCQDQNGKACMEGMMGEBCKQAVCKQGCNLLHGCSVPGECKCHYGWQG	240						
Qy	260	LYCDKCIPIHPCVHGI CNEPWOCLCETNWGQQLCDKOLANYCGTHQPCPLNGGTCSENTGDK	311						
Db	241	QYCDCEVRYPCAHSGCNEPWOCCETNWGGLLCNKLNYCGNHHPCLNGGTGCMNTEPDE	300						
Qy	320	YOCSCPEGYSGPCEIAEHAHCLSDPCNHRGSKETSLSGFCECSPGWTGPTCSNINDDCS	379						
Db	301	YRCACPDGYSKNCIEIAHACVSNPCANGTTCHEISSFKCHCPSGSGPTCAIDIDECA	360						
Qy	380	PNNCSHGTCODLVNGFKCVCPQWTGKTOLDANECEAKPCVNAKSKNLIASYYDCDL	439						
Db	361	SNPCAOGGTCTIDHINSFECICPOQWIGATCOLDANECEGKFCVNAYSKNLGGYCDCI	420						
Qy	440	PWMGQNCIDININDCLGQONDASCRDLVNGYRICPPGYAGDHCERIDDECA SNPCPLNG	499						
Db	421	PWKGVNCHININDCHGQCQHGCTCKDBVNDYHCICPRGFTGKNCETETNECESNPQNG	480						
Qy	500	GHCQNEINRFOCIPTGFSGNLCQLDIDYCEPNPCQNGCAQCYNRPASDYFKCKPREDYEGKN	559						
Db	481	GRCKDLVNGFTCLCAQGFSGVFCBMDIDFCBPNPCQNGAKCYDLGGDYCYACPDYDGN	540						
Qy	560	CSHLKDHCRTRTPCEVIDSCTVMAASNDTPEGVRVYISSNVCPGHCKCKSQSGKFTCDCKN	619						
Db	541	CSHLKDHCKNNSKVILDSCTIEVFSNTTQEGIRFISSNVCGPHGRCISQPGENFTCADR	600						
Qy	620	GFTGTYCHENINDCESNPRNGGTCIDGVNSYKICICSDGMWEGAYCETNINDCSQNPCHNG	679						
Db	601	GFTGTYCHENINDCLGPKCKNGGTCIDEVDSFKFCSSGMWEGELCDTNFNDCSNPQCHNG	660						
Qy	680	GTCRDLVNDFYCDCKNGWKGTCHRSRUSCDDEATCNNGGTCYDEGDAFKCMKCPGWGGTT	739						
Db	661	GRCLDLVNDFYCECKNDWKGTCHRSRYQCDANTCSNGGTCYDDGDTFHCSCPPEWGST	720						
Qy	740	CNIARNSCLPNPCHNGGTCVVGNGESTFCVCKEGWEGPICAONTNDCSPHPCYNSGTCVD	799						
Db	721	CNIAKNSCIPNCPWNGGTCVSGSDSPFCICKEWEGRTCTQNTNDCNPHCPYNGGICVD	780						
Qy	800	GDNWYRCECAPGFPAGPCRININCOSSPCAFGATCVDEINGYRCVCPPGHSGAKCQEV-	858						
Db	781	GVNWFRCECAPGFPAGPCRINIDECOSSPCGYGATCIDEINGYRCTCPPRGRVGRPCQBEI	840						
Qy	859	-SGRPCTIMGSVIPDGAKWDDDCNTCCQLNGRIACSKVWCGRPCLLHK-----GHSBCPS	913						
Db	841	GIGKPCWLKGMTFPHGSRWDOECNSCHCLDGRIDCTKWKVCKGKPCLLHKHWDNSNYQCPM	900						
Qy	914	GOSCIPIILDQCFVHPCTGTGCECRSSSIQPVKTKTSDSYQDNCANIPTFNKEMWSP	972						
Db	901	GQECQEKY-MKCFHPCTEWGECASBPPLANIIRLPSNGVLDNDNCARITLIFNGKNVPQ	959						
Qy	973	GLATTEHICSELRLNLIKNSABYSYIATCEPSPSANNEIHVAISABDIRD--DGNPIKE	1030						
Db	960	GTTTESICSEIRYLPATSVSRDRLIILCDLSTYSENAVEAISFPVHRDEQDNLQION	1019						
Qy	1031	ITDKIIDLVKRCQGNSSLIAAAVEVRVQ	1058						
Db	1020	AANIIVNAVTKRO-NSTWMLAVTEVKVE	1046						

Query Match	60.74	Score 3795.5	DB 2	Length 1254
Best Local Similarity	58.08	Pred. No. 4.3e-249		
Matches	622	Conservative 171	Mismatches 255	Indels 25
Qy	7	RGSGRPLSLLALLCALRAKVCASQCFLEILSMONVNGELQNGCCGARNPGDKC	66	
Db	6	RIRNLPLA---CLLLTMTWKVSQSSGFYELQIAVENVNGELWDGECDSRNSQDRC	62	
Qy	67	TRDECPTYFKVCLKEYOSRVTAGPSCSFGSGSTPVIIGNTFNLKA-----SRGNDNRIV	121	
Db	63	VRDECPTYFKVCLKEYQSEVTTTQCTFGSGSTDVLGNIFFSKTAKNSPKTSDVKII	122	
Qy	122	LPFSFAWPRSYTLVLRAWDSNSTVQ--PSDIETKASHSGMINPSRQWTLKQNTGVAHF	179	
Db	123	IPFHFRAWPRSYTLILEAWDNWDSNTQNNNGENLIERHIASHMVNPGDHWQIRHPGTAHI	182	
Qy	180	EYQIRVTCDDYYGFGCNKFCRRDDDPFGHVACDQNGKTCMEGWPCENRAICROGCS	239	
Db	183	EYRIRVRCDENYIGSKCNKQCRPDDYFGRYCDPSGNI VCLDGNWGEDCKTALCKQCN	242	
Qy	240	PKHGSKCLPGDRCQYWGQGLYCDKCIPIHFGCVHGI CNEPWCQLCETNWWGSQLCDKOLNY	299	

Db 243 LIHGCAVPCECKNTYGMWQGFCDCECLPYFGLHGTCTVMPWQCTCEKNWGLLCKDLNY 302

Qy 300 CGTHQPCNLNGTCTNTGPKYQSCPEGYSGPNCETAEHACLSDPCHNRGSCKETSLGPE 359

Db 303 CGTHPCVNGTCTMNSPEYDNCACPEGYSGKNCETAEHACVSNPCANGGTCTHEVPTGFE 362

Qy 360 CEGSPGWGTCTSTNIDDCSPNNCSHGCTCODLVNGFKVCPCPPQWTGKTQOLDANECEAK 419

Db 363 CHCPGWEGFTCAKMDDECASSPCAQGTCTDLENGFECVCPQWVGKTCQIDANECEAK 422

Qy 420 PCVNAKSKNLIASYYCDCLPGWGMQNCININDLQCGQNDASCRDLN- GYRCICPPG 478

Db 423 PCVNAHCKNMI GGYHCDCFQWAGQNCINLNGCHGQCGATCKELVHGYYHCQCPAG 482

Qy 479 YAGDHCEERDIDECASNPLNGHCHGCHVILDSFVCECPNSYAGMLCEVESLSHPNCEPNC 534

Db 483 FVGLHCEVSRNKASGFCQNGRCHVILDSFVCECPNSYAGMLCEVESLSHPNCEPNC 542

Qy 535 QNGAQCYNRASDYFCKPEDEYGNKCSHLKHCHRTTPEVIDTCTVAMASNDTPEGVRYI 594

Db 543 QNTALCYSLPGDFYACPEDEYGTCTENRKHCHRTTPEVIDTCTVAMASNDTPEGVRYI 602

Qy 595 SSNVCGPHGCKKSQSGKFTCDCKMGFTGTGTCHENINDCESNPCRNGGTCTIDGVNSYKCI 654

Db 603 NSNVCGPHGCKKSQSGKFTCTCELGTGTGTCHENVNDCVSNPCRNGGTCTIDGVNSYKCI 662

Qy 655 CSQWEGAYCETNINDCSQNPCHNGTCTRLVNDFYCDCKNGKWKGTCHSRDQCDATC 714

Db 663 CPDQWEGDLCSINYNESRSPCKNGRCHVILDSFVCECEANGWKGTCHSRDQCDSTC 722

Qy 715 NNGTCYDDEGAPKCPGWEGTCTNARNSSCLPNPCHNGTCTVNGGSEFTCVCKEGW 774

Db 723 SNGTCTYDHDGAPKCPGWEGTCTNARNSSCLPNPCHNGTCTVNGGSEFTCVCKEGW 782

Qy 775 EGPICATQNTDCSPHPCYNSGTCVDGNWYRCECAPGAGFAGDPCRININEQSSPCFARGAT 834

Db 783 EGATCAQNTDCNHPHPCYNGGICVDGNWYRCECAPGAGFAGDPCRININEQSSPCFARGAT 842

Qy 835 CVDBINGYRCVCPGHSAGKQEV- -SGRPCITWGSVIPDGAQWDDCNTCQNLNRIAC 892

Db 843 CVDBINGYRCVCPGHSAGKQEV- -SGRPCITWGSVIPDGAQWDDCNTCQNLNRIAC 902

Qy 893 SKWCGPRPCLL- -HKGHSECPGSGOSCPILDQCFVHPCTGVGECRSSLQ- -VKTK 947

Db 903 TKVCGRKPCLLPTGPRELHYCGGECLEHNFCLTCLPCHQWGFCSPEPTLTQTK 962

Qy 948 CTSDSYQD- -NCANITFTFNKEMSPGLTTEHICSELRLNINLKVSAEYSIYIACPPSP 1006

Db 963 CEPNSVYLDKSCARITLIFNRDLPTGTTVENVCSLRYPATRSIAKDKHLLVLCDSL 1022

Qy 1007 SANNEIHWASAE- -DIRDDGNPIKEITDKIIDLVSKRDNSSLLIAAVERVQ 1058

Db 1023 KNODAVEVAISFOHDEQPSHSQIOEAASTIVSTLSKRH- -NSTVMIAVIEVKVE 1074

RESULT 13

Q5TZK8\_BRARE PRELIMINARY; PRT; 1254 AA.

ID Q5TZK8 BRARE PRELIMINARY; PRT; 1254 AA.

AC Q5TZK8; AC

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Jagged2.

GN Name=Jag2; ORFNames=DK5Y-5P1.1-001;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_taxid=7955;

RN NUCLEOTIDE SEQUENCE.

RA Corby N.;

RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX004766; CAH69087.1; -; Genomic\_DNA.

DR GO; GO:0016020; C-membrane; IEA.

DR GO; GO:000509; F-calciun ion binding; IEA.

DR GO; GO:0007154; P-cell communication; IEA.

DR InterPro; IPR000152; Asx\_hydroxyl\_S.

DR InterPro; IPR001174; DSL.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001438; EGF\_II.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR011651; MNHL.

DR InterPro; IPR006552; VWC out.

DR InterPro; IPR001007; VWF\_C.

DR Pfam; PF01414; DSL; 1.

DR Pfam; PF00008; EGF; 14.

DR Pfam; PF07645; EGF\_CA; 1.

DR Pfam; PF07657; MNHL; 1.

DR Pfam; PF00093; VWC; 1.

DR PRINTS; PR00010; EGFLOOD.

DR SMART; SM00051; DSL; 1.

DR SMART; SM00181; EGF; 16.

DR SMART; SM00179; EGF\_CA; 14.

DR SMART; SM00215; VWC\_out; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; 7.

DR PROSITE; PS00022; EGF\_1; 16.

DR PROSITE; PS01186; EGF\_2; 11.

DR PROSITE; PS00026; EGF\_3; 15.

DR PROSITE; PS01187; EGF\_CA; 6.

SQ SEQUENCE 1254 AA; 137623 MW; D546358F912C9FFA CRC64;

Query Match 60.7%; Score 3790.5; DB 2; Length 1254;

Best Local Similarity 57.9%; Pred. No. 9.3e-249;

Matches 621; Conservative 171; Mismatches 256; Indels 25; Gaps 11;

Qy 7 RGRSGRLPALLALLCALRAKVCASGQPELEILSMQNVGELQNGCCGARNPGDRKC 66

Db 6 RIRNLPPIA- -CLLLTMTWKVSQSSGYPELQLIAVENNVGELWDGECDDSTRNSQDRC 62

Qy 67 TRDECTYFKVCLKEVQSRVTAGCPGSGSPVIGGTFNLKA- - - - -SRGNDNRIV 121

Db 63 VRDECTYFKVCLKEVQSEVTTTQCTFGSGSTDLVGLGIIISFKTAKNSPKSTSDVGKII 122

Qy 122 LPFSFAWPRSYTLLEAWDSSNDTVQ- -PDSIIIEKASHSGMINPSPROWTLKONTGVAFH 179

Db 123 IPFHFAWPRSYTLLEAWDSSNDTVQ- -PDSIIIEKASHSGMINPSPROWTLKONTGVAFH 182

Qy 180 EYQIRVTCDYVYFGCNKFCRPRDDPFPHYACQDQNGKTCMBGWMGPECNRAICRGCS 239

Db 183 EYRIRVRCDENYYSKCNKQCRPRDDPFPHYACQDQNGKTCMBGWMGPECNRAICRGCS 242

Qy 240 PKHGSCKLPDRCQYQWQGLYCDKCIIPHGCVHIGICNEPWOCLCEINWGGQLCDKDLNY 299

Db 243 LIHGCAVPCECKNTYGMWQGFCDCECLPYFGLHGTCTVMPWQCTCEKNWGLLCKDLNY 302

Qy 300 CGTHQPCNLNGTCTNTGPKYQSCPEGYSGPNCETAEHACLSDPCHNRGSCKETSLGFE 359

Db 303 CGTHPCVNGTCTMNSPEYDNCACPEGYSGKNCETAEHACVSNPCANGGTCTHEVPTGFE 362

Qy 360 CEGSPGWGTCTSTNIDDCSPNNCSHGCTCODLVNGFKVCPCPPQWTGKTQOLDANECEAK 419

Db 363 CHCPGWEGFTCAKMDDECASSPCAQGTCTDLENGFECVCPQWVGKTCQIDANECEAK 422

Qy 420 PCVNAKSKNLIASYYCDCLPGWGMQNCININDLQCGQNDASCRDLN- GYRCICPPG 478

Db 423 PCVNAHCKNMI GGYHCDCFQWAGQNCINLNGCHGQCGATCKELVHGYYHCQCPAG 482

Qy 479 YAGDHCEERDIDECASNPLNGHCHGCHVILDSFVCECPNSYAGMLCEVESLSHPNCEPNC 534

Db 483 FVGLHCEVSRNKASGFCQNGRCHVILDSFVCECPNSYAGMLCEVESLSHPNCEPNC 542

Qy 535 QNGAQCYNRASDYFCKPEDEYGNKCSHLKHCHRTTPEVIDTCTVAMASNDTPEGVRYI 594



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QY 715 NNGGTCYDEGDAKCKPCGGWEGTTCNIARNSSCLPNPCHNGCTCVVNGESFTCVCKEGW 774
Db 723 NNGGTCYDHDGAFRCACPPCGWEGSTCTAKNSTCASGCLNGCTCVGGGDTFTCI CKDGG 782
QY 775 EGPICANTQNDSCPHPCYNCGTCDGDNWYRCAPAGFAGPDCRININEQSSPCAFAGAT 834
Db 783 EGATCAQNTDNDPHPCYNGGICVDGWNWRCAPAGFAGPDCRININEQSSPCAYGAT 842
QY 835 CVDEINGYRCVCPGHSAGKQEV--SGRPCITGWSVIPDGAKWDDCNTCQCLNGRIAC 892
Db 843 CVDEINGYRCVPLRGTPQCFIGIGTKCHVAGLQFPHGSWEBCNCTCQCVNGKVEC 902
QY 893 SKWCGRPCLL-----HKHSECPSCGSCIPILDDQCFVHPCTGVGECRSSSLQP-VKTK 947
Db 903 TKVCGRKPCLLPTGPTRGLHYCPGGRECLHFLTCLSPCHQWGFCSPPETPTLQTK 962
QY 948 CTSDSYYQD--NCANITFTFNKEMWSPGLTTEHCSELNRLNKNVSAEYSIYIACEPSP 1006
Db 963 CEPNSVLDKSCARITILFNDRKLPPTGTTVENVCSELRYMPATRESLAKDKHLVLCDLSY 1022
QY 1007 SANNEIHVAISAE--DIRDDGNPKIEITDKIIDLVSXKRDGNSSLIAAVALVRVQ 1058
Db 1023 KNQDAVEVAISFQHDQEPQSHSQIEAAASTIVSTLSKRH-NSTVMLAVIEVKVE 1074

RESULT 15
JAG2 HUMAN
ID --JAG2 HUMAN STANDARD; PRT; 1238 AA.
AC Q9Y219; Q9UE17; Q9UE99; Q9UNK8; Q9Y6P9; Q9Y6Q0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Jagged-2 precursor (Jagged2) (HJ2).
GN Name=JAG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RX MEDLINE=97459705; PubMed=93115665;
RA Luo B., Aster J.C., Haasler J.R., Kuo F., Sklar J.;
RT "Isolation and functional analysis of a cDNA for human Jagged2, a gene
RT encoding a ligand for the Notch1 receptor."
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RC TISSUE=Fetal brain;
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.;
RT "Human ligands of the Notch receptor."
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT).
RC TISSUE=Bone marrow;
RX MEDLINE=20130121; PubMed=10662552; DOI=10.1006/geno.1999.6045;
RA Deng Y., Madan A., Banta A.B., Friedman C., Trask B.J., Hood L.,
RA Li L.;
RT "Characterization, chromosomal localization, and the complete 30-kb
RT DNA sequence of the human Jagged2 (JAG2) gene."
RN [4]
RP NUCLEOTIDE SEQUENCE OF 17-1238 (ISOFORM LONG).
RC TISSUE=Heart;
RX MEDLINE=98145947; PubMed=9486542; DOI=10.1016/S0925-4773(97)00146-9;
RA Valsecchi C., Ghezzi C., Ballabio A., Ruggeri E.I.;
RT "JAGGED2: a putative Notch ligand expressed in the apical ectodermal
RT ridge and in sites of epithelial-mesenchymal interactions."
RN [5]
CC Mech. Dev. 69:203-207(1997).
CC -!- FUNCTION: Putative Notch ligand involved in the mediation of Notch
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KW Alternative splicing; Calcium; Developmental protein; EGF-like domain;  
KW Glycoprotein; Notch signaling pathway; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 26 Potential.  
FT CHAIN 27 1238 Jagged-2.  
FT TOPO\_DOM 27 1080 Extracellular (Potential).  
FT TRANSMEM 1081 1105 Potential.  
FT TOPO\_DOM 1106 1238 Cytoplasmic (Potential).  
FT DONAIN 196 240 DSL.  
FT DONAIN 241 274 EGF-like 1.  
FT DONAIN 275 305 EGF-like 2.  
FT DONAIN 307 345 EGF-like 3.  
FT DONAIN 347 383 EGF-like 4.  
FT DONAIN 385 421 EGF-like 5; calcium-binding (Potential).  
FT DONAIN 423 459 EGF-like 6; calcium-binding (Potential).  
FT DONAIN 461 496 EGF-like 7; calcium-binding (Potential).  
FT DONAIN 498 534 EGF-like 8.  
FT DONAIN 536 572 EGF-like 9.  
FT DONAIN 574 634 EGF-like 10; atypical.  
FT DONAIN 636 672 EGF-like 11; calcium-binding (Potential).  
FT DONAIN 674 710 EGF-like 12; calcium-binding (Potential).  
FT DONAIN 712 748 EGF-like 13.  
FT DONAIN 751 787 EGF-like 14.  
FT DONAIN 789 825 EGF-like 15; calcium-binding (Potential).  
FT DONAIN 827 863 EGF-like 16; calcium-binding (Potential).  
FT DONAIN 870 944 WFC.  
FT CARBOHYD 153 153 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 570 570 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 619 619 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 752 752 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 1058 1058 N-linked (GlcNAc. . .) (Potential).  
FT DISULFID 245 256 By similarity.  
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FT DISULFID 562 571 By similarity.  
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FT DISULFID 645 660 By similarity.  
FT DISULFID 662 671 By similarity.  
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FT DISULFID 716 727 By similarity.  
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FT DISULFID 738 747 By similarity.  
FT DISULFID 755 766 By similarity.  
FT DISULFID 760 775 By similarity.  
FT DISULFID 777 786 By similarity.  
FT DISULFID 793 804 By similarity.

FT DISULFID 798 813 By similarity.  
FT DISULFID 815 824 By similarity.  
FT DISULFID 831 842 By similarity.  
FT DISULFID 851 862 By similarity.  
FT DISULFID 853 862 By similarity.  
FT VARSPLIC 424 461 Missing (in isoform Short).  
FT CONFLICT 8 12 /FTID=VSP\_001395.  
FT CONFLICT 119 119 RLPID -> APPPA (in Ref. 1).  
FT CONFLICT 119 119 A -> P (in Ref. 1).  
Query Match 59.0%; Score 3685; DB 1; Length 1238;  
Best Local Similarity 57.3%; Pred. No. 1.3e-241;  
Matches 619; Conservative 153; Mismatches 272; Indels 36; Gaps 13;  
QY 5 RTRGRGRPLSLALLCALRAKVCASGQFELILSMQNVGELQNGCC-GEARNPGD 63  
DB 2 RAQGRGLRRL--LJLLALWQAARPMGYFELQLSALRVNVELLSGACDGDGRTRA 59  
QY 64 RKTRDECDTYFKVCLKEYQSRVTAGGPCSGFGSGTPTVGGTFFNL-----KA 111  
DB 60 GGCCHDECDTYVRVCLKEYQAKVTPTGPCSYGHGATPVLGNSFYLPAGAGDRARARA 119  
QY 112 SRGNDRN--RIVLPFSFAMPRSYTLLEAWDSSNDTV-OPDSIIERKASHGMINPSQWQ 168  
DB 120 RAGGDQDPLGLVTPQFAMPRSFLLIVEAWDNDTTPNEELLIERVSHAGMINPDRWK 179  
QY 169 TLKQNTGVAHFQIRVTCDYVYFGCNKFCRPRDDFFGHYACDQNGNKTCEGWMGPE 228  
DB 180 SLHFSGHVAHLELIQIRVCDENYYSATCNKFCRPRDDFFGHYTCDOYGNKACMDGWMGKE 239  
QY 229 CNRAICRQCSKPKHGSCKLPGDCRCQYWGQGLYCDKCIPIHPGCVHGINPWCCLCTNW 288  
DB 240 CREAVCKQGNLLHGGCTVPGECRCSYGWQRCDECVYPGCVHSGCVPMQNCSTNW 299  
QY 289 GGQLCDKDLNYCGTHOPCLNGGTCNTGDKYCSGPEGYSNGCETAEHACISDPCHNR 348  
DB 300 GGLLCDKDLNYCGSHHPCTNGGTCINAEPPQVRCCTPDGYSGRNCKAEHACTSNPCANG 359  
QY 349 GSCKETSLGFECECSFGWTGPTCSTNIDDCSNPNCSHGTCQDLVNGFKVCVCPQMTGKT 408  
DB 360 GSCEVPSGFECHCPSGMSGPTCALDIDECASNPCAAGTCVDQVDGFEICPEQWVGAT 419  
QY 409 QOLDANECAKPCVNAKSKNLIASYYCDCLPGWMQNCQDININDCLGQCNDAASCDLV 468  
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QY 469 NGYRCICPGYAGDHCEERIDECASNPLCLNGHGCQNEIRFQCLCPTGSEGNLCQDIDY 528  
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QY 529 CEPNPNQGAQCYNRASDYFCKPEDYEGKNCNKLKDHCRTPTEVIDSCVTAMASNDTP 588  
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QY 589 EGVYIISNVCGPHGKCSQSGKFTCDNKGFTGYCHENINDCSNPNCRNGGTCDGV 648  
DB 596 GMPGTAASGVCGPHGRCVSPQGNFSCI CDGSGTGYCHENIDCLGQPCRNNGTCDIEV 655  
QY 649 NSYKCI CSQGWEGAYCETINIDCSQNPCHNGGTCRDLVNDYCDCKNGWKGTCHSRDSQ 708  
DB 656 DAFCRCPSGWEGLCDTNPNDCLPDPCHSRGRCYDLVNDYFACDDGDKWKGTCHSRFQ 715  
QY 709 CDEATCNGGTCYDEGDAFKCMCPGWEGTTCNIARNSSCLPNPCHNGGTCVNVNGSFTC 768  
DB 716 CDATCSNGGTCYDSGDTFRACPPGWKSTCAVAKNSCLPNPCVNGGTCVSGSASFSC 775  
QY 769 VCKBGEPICAQNTNDCSPHPCYNSGTCTVDGNWYRCBAPGAFAGDCRININEQOSSP 828  
DB 776 ICRDGEWGRCTHTNTDNCNPLCYNGGICVDGWNWFRCECAPGAFAGDCRINIDECOSSP 835  
QY 829 CAFGATCVDEINGYRCVCPPHSGAKCOEV--SGRPIITMGSVIPDGAKWDDDCNTCQCL 886  
DB 836 CAYGATCVDEINGYRCVCPPHSGAKCOEV--SGRPIITMGSVIPDGAKWDDDCNTCQCL 895

Qy	887	NGRIACSKVWCGPRPCLLLHKGHSE-----CPSGQSCIPILDDQCFVHPCTGVGECRSSSL	941
Db	896	DGRRDCSKVWCGWKPCLL-AGQPEALSAQCPLGQRCLEKAPGQCLRPPCEAWGECGAE--	952
Qy	942	QPVKTKCTSDSYOD-NCANITFTENKEMMSPLTTEHICSELNRLNLIKNVSAEYSIVI	1000
Db	953	EPPSTPCLPBSGHLDDNNCARLTLHFNRDHVPQGTTVGALCSGIRSLPATRAVARDRLVL	1012
Qy	1001	ACEPSPSANNEIHVAISAEDIRD--DGNPIKEITDKIIDLVSKRDGNSSLIAAAVAVRVQ	1058
Db	1013	LCDRASSGASAVEVAVSFSPARDLPDSSLIQGAHAIVAIAITQR-GNSSLLLAATEVKVE	1071

Search completed: February 4, 2006, 09:35:31  
Job time : 276 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 09:06:39 ; Search time 645 Seconds  
(without alignments)  
10078.361 Million cell updates/sec

Title: US-10-650-650-2

Perfect score: 3655.8

Sequence: 1 atcgcttccacgacrcg.....gaatggatcatcgtagatg 3657

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing files: 45 summaries

Database : Issued Patents NA\*

- 1: /cgn2\_6/prodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq.\*
- 7: /cgn2\_6/prodata/1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3655.8	100.0	3657	3	US-09-579-536C-2
2	3654.2	99.9	5590	3	US-08-882-046-1
3	3654.2	99.9	5590	3	US-09-566-047-1
4	3654.2	99.9	5896	3	US-09-949-016-31
5	3651	99.9	4208	3	US-09-068-740A-10
6	3651	99.9	5885	3	US-09-949-016-4426
7	3649.4	99.8	4855	3	US-09-917-254-34
8	3647.8	99.8	4208	3	US-09-214-278-6
9	3647.8	99.8	4208	3	US-09-855-722-6
10	3646.2	99.7	6464	2	US-08-400-159-5
11	3646.2	99.7	6464	3	US-08-611-729A-5
12	3646.2	99.7	6464	3	US-09-195-524-5
13	3646.2	99.7	6464	3	US-09-310-685-3
14	3611.8	98.8	5458	3	US-09-199-865-2
15	3611.8	98.8	5458	3	US-10-213-329-2
16	3199.8	87.5	3201	3	US-09-579-536C-17
17	2455.4	67.2	3582	2	US-08-400-159-9
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22	1157.8	31.7	3955	3	US-09-855-722-4
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24	1056.4	28.9	4483	3	US-09-195-524-7

ALIGNMENTS

RESULT 1

US-09-579-536C-2

Sequence 2, Application US/09579536C

Patent No. 6716974

GENERAL INFORMATION:

APPLICANT: MACIAG, Thomas

APPLICANT: ZIMRIN, Ann

APPLICANT: SMALL, Deena

APPLICANT: PRUDOVSKY, Igor

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG

TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE: 053689-5002-01

CURRENT APPLICATION NUMBER: US/09/579,536C

CURRENT FILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 09/199,865

PRIOR FILING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: PCT/US97/09407

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/018,841

PRIOR FILING DATE: 1996-05-31

NUMBER OF SEQ ID NOS: 56

SOFTWARE: Patent in version 3.1

SEQ ID NO 2

LENGTH: 3657

TYPE: DNA

ORGANISM: Homo sapiens

US-09-579-536C-2

Query Match 100.0%; Score 3655.8; DB 3; Length 3657;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGTTCCTCCACGGACRCGCGCGCTCGGGCGCCCTAGAGCTCTGCTCGCCCTG 60

Db 1 ATCGTTCCTCCACGGACRCGCGCGCTCGGGCGCCCTAGAGCTCTGCTCGCCCTG 60

QY 61 CTCTGTGCTTCGAGCCAAAGTGTGTGTGGGCTCGGGCTCGAGTTGAGATCCTG 120

Db 61 CTCTGTGCTTCGAGCCAAAGTGTGTGTGGGCTCGGGCTCGAGTTGAGATCCTG 120

QY 121 TCATGCGAAGCTGAAACGGGAGCTGCGAGAACTGTGCGCGCGCGCCGCGAAC 180

Db 121 TCATGCGAAGCTGAAACGGGAGCTGCGAGAACTGTGCGCGCGCGCCGCGAAC 180

QY 181 CCGGAGACCGCAAGTGCACCCCGGAGTGTGACATACCTCAAGTGTGCTCAAG 240

Db 181 CCGGAGACCGCAAGTGCACCCCGGAGTGTGACATACCTCAAGTGTGCTCAAG 240



QY	241	GAGTATCAGTCCGCGTCA	CGGCGGGGGGSCCTTG	CAGCTTCGGCTCAGGGTCCA	CGCCT	300
Db	241	GAGTATCAGTCCC	CGCGTCA	CGGCGGGGGGSCCTTG	CAGCTTCGGCTCAGGGTCCA	CGCCT
QY	301	GTATCGGGGGCAACACCTT	CAACCTCAAGCCAGCGCGGCAAC	GACCGCAACCGCATC		360
Db	301	GTATCGGGGGCAACACCTT	CAACCTCAAGCCAGCGCGGCAAC	GACCGCAACCGCATC		360
QY	361	GTCTGCTTTTCA	GTTCGGCTGGCGAGGTCTCTA	TCAGTTGCTTGTGAGGGCGTGGAT		420
Db	361	GTCTGCTTTTCA	GTTCGGCTGGCGAGGTCTCTA	TCAGTTGCTTGTGAGGGCGTGGAT		420
QY	421	TCCAGTAA	TGACACCGTTCAACCTGACAGTATTTG	MAAGGCTTCTCACTCGGCGATG		480
Db	421	TCCAGTAA	TGACACCGTTCAACCTGACAGTATTTG	MAAGGCTTCTCACTCGGCGATG		480
QY	481	ATCAACCCCA	CGCGGAGTGGCAGACGCTGA	GCAGAAACCGGGCGTGGAG		540
Db	481	ATCAACCCCA	CGCGGAGTGGCAGACGCTGA	GCAGAAACCGGGCGTGGAG		540
QY	541	TATCAGATCCG	GTGACCTGTGATGACTACTA	TATGGCTTTGGCTGYAATAAGTTCTGC		600
Db	541	TATCAGATCCG	GTGACCTGTGATGACTACTA	TATGGCTTTGGCTGYAATAAGTTCTGC		600
QY	601	CGCCCGAGATGACTTCT	TTGGACACTATGCCCTGTGACCAGAA	TGGCAACAAACTTGC		660
Db	601	CGCCCGAGATGACTTCT	TTGGACACTATGCCCTGTGACCAGAA	TGGCAACAAACTTGC		660
QY	661	ATGGAAGGCTTGGAT	TGGGCCCGGAATGTAACAGAGCTATTT	TGCCGACAAGGCTCGAGTCT		720
Db	661	ATGGAAGGCTTGGAT	TGGGCCCGGAATGTAACAGAGCTATTT	TGCCGACAAGGCTCGAGTCT		720
QY	721	AAGATGGGTCTTGCA	AACTCCACAGTGA	CTGACAGTGCAGTAYGGCTGGCAAGGCTG		780
Db	721	AAGATGGGTCTTGCA	AACTCCACAGTGA	CTGACAGTGCAGTAYGGCTGGCAAGGCTG		780
QY	781	TACTGTATAGTGCAT	CCACACCGGGATGGTCCACGGCATCT	GTATAGACCTGG		840
Db	781	TACTGTATAGTGCAT	CCACACCGGGATGGTCCACGGCATCT	GTATAGACCTGG		840
QY	841	CAGTGCTCTGTGAG	ACCACTGGGCGGCAGCTCTGTGACAA	AGATCTCAATTACTGT		900
Db	841	CAGTGCTCTGTGAG	ACCACTGGGCGGCAGCTCTGTGACAA	AGATCTCAATTACTGT		900
QY	901	GGGACTCATAG	CGCGTGTCTCAACGGGGGAAC	CTTTGTAGCAACACAGGCGCTGACAAATAT		960
Db	901	GGGACTCATAG	CGCGTGTGTCTCAACGGGGGAAC	CTTTGTAGCAACACAGGCGCTGACAAATAT		960
QY	961	CAGTGTTCCTG	CGCTGAGGGGTATTCAGGACCCAACTGT	GAAATTGCTGAGCACGCGCTGC		1020
Db	961	CAGTGTTCCTG	CGCTGAGGGGTATTCAGGACCCAACTGT	GAAATTGCTGAGCACGCGCTGC		1020
QY	1021	CTCTCTGATCCCTGT	CAACAAGGCGAGCTGTAAAGGAGAC	TCCCTCGGCTTTGAGTGT		1080
Db	1021	CTCTCTGATCCCTGT	CAACAAGGCGAGCTGTAAAGGAGAC	TCCCTCGGCTTTGAGTGT		1080
QY	1081	GAGTGTTC	CGGCTGGACCGGCCCCACATGCTCTA	CAACATTTGATGACTGTTCCT		1140
Db	1081	GAGTGTTC	CGGCTGGACCGGCCCCACATGCTCTA	CAACATTTGATGACTGTTCCT		1140
QY	1141	AATAACTGTTCC	ACAGGGGACCTGCGAGGACCTGGT	TAAACGATTTAAGTGTGTGTC		1200
Db	1141	AATAACTGTTCC	ACAGGGGACCTGCGAGGACCTGGT	TAAACGATTTAAGTGTGTGTC		1200
QY	1201	CCCCCAGTGG	ACTGGGAAAACGTGCGAGTTAGATG	CAAAATGAAATGAGGGCAAACT		1260
Db	1201	CCCCCAGTGG	ACTGGGAAAACGTGCGAGTTAGATG	CAAAATGAAATGAGGGCAAACT		1260
QY	1261	TGTGTAA	CGGCAAACTCTGTGAAGATCTCAT	TTCGCGAGCTACTCTCGGACTGTCTCC		1320
Db	1261	TGTGTAA	CGGCAAACTCTGTGAAGATCTCAT	TTCGCGAGCTACTCTCGGACTGTCTCC		1320

QY	1321	GGCTGATGGGT	CAGAAATGTGACATAAATATTAAT	AGACTGCTTGGCCAGTGTCAGAAT		1380
Db	1321	GGCTGATGGGT	CAGAAATGTGACATAAATATTAAT	AGACTGCTTGGCCAGTGTCAGAAT		1380
QY	1381	GACGCTCTCT	CGGATTTGGTTAATGGTTATCG	CTGTATCTGTCCACTGCTATGCA		1440
Db	1381	GACGCTCTCT	CGGATTTGGTTAATGGTTATCG	CTGTATCTGTCCACTGCTATGCA		1440
QY	1441	GGGATCACT	GTGAGAGACATCGATGAATGT	GCCAGCAACCCCTGTTTGAATGGGGT		1500
Db	1441	GGGATCACT	GTGAGAGACATCGATGAATGT	GCCAGCAACCCCTGTTTGAATGGGGT		1500
QY	1501	CACGTGCA	AGTAAATCAACAGATTC	CAGTGTCTGTGCCCACTGTTCTCGAAAC		1560
Db	1501	CACGTGCA	AGTAAATCAACAGATTC	CAGTGTCTGTGCCCACTGTTCTCGAAAC		1560
QY	1561	CTCTGAC	GTGACATCGATTTGTGAGCCTAAT	TCCTGCCAGAACGGTGCCAGTGC		1620
Db	1561	CTCTGAC	GTGACATCGATTTGTGAGCCTAAT	TCCTGCCAGAACGGTGCCAGTGC		1620
QY	1621	TACAA	CGGTGCCAGTCACTATTTCT	GCAAGTGCCTGAGGACTATGAGGSCAAGAACTGC		1680
Db	1621	TACAA	CGGTGCCAGTCACTATTTCT	GCAAGTGCCTGAGGACTATGAGGSCAAGAACTGC		1680
QY	1681	TACACCT	GAAAGACCACTGCCG	CACGACCCCTGTGAAAGTGAATTGACAGCTGCACAGTG		1740
Db	1681	TACACCT	GAAAGACCACTGCCG	CACGACCCCTGTGAAAGTGAATTGACAGCTGCACAGTG		1740
QY	1741	GCATGGCTT	CCAAACACACCTG	AAAGGGTGGGTATATTTCTTCC	TCCAAAGTCTGTGGT	1800
Db	1741	GCATGGCTT	CCAAACACACCTG	AAAGGGTGGGTATATTTCTTCC	TCCAAAGTCTGTGGT	1800
QY	1801	CCTCAG	GGAAGTGAAGTCACTG	CGGAGGCAAAATTCACCTGTGACTGTCTAACAAGGC		1860
Db	1801	CCTCAG	GGAAGTGAAGTCACTG	CGGAGGCAAAATTCACCTGTGACTGTCTAACAAGGC		1860
QY	1861	TTCA	CGGGAACATAC	TGCCATGAAAAATATTAAT	GAAGTGTGAGAGCAACCCCTGTGAGAAAC	1920
Db	1861	TTCA	CGGGAACATAC	TGCCATGAAAAATATTAAT	GAAGTGTGAGAGCAACCCCTGTGAGAAAC	1920
QY	1921	GGTGG	CACTTGCATCGATGGTGC	AACTCTCAAGTGCATCTGTAGTGA	CGGCTGGGAG	1980
Db	1921	GGTGG	CACTTGCATCGATGGTGC	AACTCTCAAGTGCATCTGTAGTGA	CGGCTGGGAG	1980
QY	1981	GGGGCT	TACTGTGAAACCAATATTAAT	GAAGTGTGAGAGCAACCCCTG	CGGAGGC	2040
Db	1981	GGGGCT	TACTGTGAAACCAATATTAAT	GAAGTGTGAGAGCAACCCCTG	CGGAGGC	2040
QY	2041	ACGTG	CGGACCTGGTCAATGACTTCT	ACTGTGACTGTAAAAATGGGTG	GAAGGAAAG	2100
Db	2041	ACGTG	CGGACCTGGTCAATGACTTCT	ACTGTGACTGTAAAAATGGGTG	GAAGGAAAG	2100
QY	2101	ACCTG	CACTCACTGACAGTGA	GTGATGAGGCAACGTCGCAACAAACGGTGGCACCTGC		2160
Db	2101	ACCTG	CACTCACTGACAGTGA	GTGATGAGGCAACGTCGCAACAAACGGTGGCACCTGC		2160
QY	2161	TATG	TAGGGGATGCTTTTAA	TGATGCTGTCTGGCGCTGGGAAGGAAACACCTGT		2220
Db	2161	TATG	TAGGGGATGCTTTTAA	TGATGCTGTCTGGCGCTGGGAAGGAAACACCTGT		2220
QY	2221	AA	CATAGCCGAAACAGTAGCT	CGCTGCCCAACCCCTGCCATTAATGGGGGCACATGTGTG		2280
Db	2221	AA	CATAGCCGAAACAGTAGCT	CGCTGCCCAACCCCTGCCATTAATGGGGGCACATGTGTG		2280
QY	2281	GTCAA	CGGCGAGTCTTTTAC	TGCTGCAAGGAGGCTGGGAGGGGCCCATCTGTGCT		2340
Db	2281	GTCAA	CGGCGAGTCTTTTAC	TGCTGCAAGGAGGCTGGGAGGGGCCCATCTGTGCT		2340
QY	2341	CAGA	TACCAATGACTG	CAGCCCTCATCTGTTTACAAAGCGGACCTGTGTGGATGGA		2400
Db	2341	CAGA	TACCAATGACTG	CAGCCCTCATCTGTTTACAAAGCGGACCTGTGTGGATGGA		2400
QY	2401	GACA	ACTGGTACCGGTG	CGAAATGTGCCCGGGTTTTGCTGGGGCCCGACTG	CGAATAAAC	2460



181 QY CCGGAGACCGCAAGTGCACCCCGGACGAGTGTGACACATCTTCAAAGTGTCCCTCAAG 240  
182 |  
183 |  
594 Db CCGGGAGACCGCAAGTGCACCCCGGACGAGTGTGACACATCTTCAAAGTGTCCCTCAAG 653  
595 |  
596 |  
241 QY GAGTATCAGTCCCGCGTCAAGCGCGGGGGCCCTGACAGCTTCCGCTCAGGGTCCAGCCCT 300  
242 |  
243 |  
654 Db GAGTATCAGTCCCGCGTCAAGCGCGGGGGCCCTGACAGCTTCCGCTCAGGGTCCAGCCCT 713  
655 |  
656 |  
301 QY GTCATCGGGGGCAACACTTCAACCTCAAGCGCAGCGCGGGCAACGACCGCAACCGGATC 360  
302 |  
303 |  
714 Db GTCATCGGGGGCAACACTTCAACCTCAAGCGCAGCGCGGGCAACGACCGCAACCGGATC 773  
715 |  
716 |  
361 QY GTGCTGCTTTTCAAGTTCGGCTGCGCGAGGTCTCTATACGTTGCTTGTGAGGGGTGGAT 420  
362 |  
363 |  
774 Db GTGCTGCTTTTCAAGTTCGGCTGCGCGAGGTCTCTATACGTTGCTTGTGAGGGGTGGAT 833  
775 |  
776 |  
421 QY TCCAGTAATGACACCGTTCAACCTGACAGTATTAATGAAAGGCTTCTCACTCGGGCATG 480  
422 |  
423 |  
834 Db TCCAGTAATGACACCGTTCAACCTGACAGTATTAATGAAAGGCTTCTCACTCGGGCATG 893  
835 |  
836 |  
481 QY ATCAACCCGAGCGGAGTGGCAGACGCTGAAGCAGAACACGGGCGTGTGCCACTTTGAG 540  
482 |  
483 |  
894 Db ATCAACCCGAGCGGAGTGGCAGACGCTGAAGCAGAACACGGGCGTGTGCCACTTTGAG 953  
895 |  
896 |  
541 QY TATCAGATCCGCGTGACCTGTGATGACTACTACTATGCGCTTGGCTGTYAATAAGTTCTGC 600  
542 |  
543 |  
954 Db TATCAGATCCGCGTGACCTGTGATGACTACTACTATGCGCTTGGCTGCAATAAGTTCTGC 1013  
955 |  
956 |  
601 QY CGCCCCAGAGATGACTTCTTTGGACACTATGCCCTGTGACAGAAATGGCAACAAACTTGC 660  
602 |  
603 |  
1014 Db CGCCCCAGAGATGACTTCTTTGGACACTATGCCCTGTGACAGAAATGGCAACAAACTTGC 1073  
1015 |  
1016 |  
661 QY ATGGAAGGCTGGATGGGCCCGCAATGTAACAGAGCTATTTTGGCGAACAGGCTGCACTCT 720  
662 |  
663 |  
1074 Db ATGGAAGGCTGGATGGGCCCGCAATGTAACAGAGCTATTTTGGCGAACAGGCTGCACTCT 1133  
1075 |  
1076 |  
721 QY AAGCATGGGTCTTGCAAACTCCAGGTGACTGCGAGGTGCCAGTAYGGCTGGCAGGCGCTG 780  
722 |  
723 |  
1134 Db AAGCATGGGTCTTGCAAACTCCAGGTGACTGCGAGGTGCCAGTAYGGCTGGCAGGCGCTG 1193  
1135 |  
1136 |  
781 QY TACTGTGATAAGTGCATCCACACCCCGGGATGGCTCCACCGGCATCTGTAATGAGCCCTGG 840  
782 |  
783 |  
1194 Db TACTGTGATAAGTGCATCCACACCCCGGGATGGCTCCACCGGCATCTGTAATGAGCCCTGG 1253  
1195 |  
1196 |  
841 QY CAGTGCCTCTGTGAGACCAACTGGGGCGCCAGCTCTGTGACAAAAGATCTCAATTACTGT 900  
842 |  
843 |  
1254 Db CAGTGCCTCTGTGAGACCAACTGGGGCGCCAGCTCTGTGACAAAAGATCTCAATTACTGT 1313  
1255 |  
1256 |  
901 QY GGGACTCATCAGCCGTGTCTCAACGGGGGAACCTGTAGCAACACAGGCCCTTGACAAATAT 960  
902 |  
903 |  
1314 Db GGGACTCATCAGCCGTGTCTCAACGGGGGAACCTGTAGCAACACAGGCCCTTGACAAATAT 1373  
1315 |  
1316 |  
961 QY CAGTGTTCCTGCCCTGAGGGGTATTCAGGACCCCAACTGTGAAATTTGTGACGACGCCCTGC 1020  
962 |  
963 |  
1374 Db CAGTGTTCCTGCCCTGAGGGGTATTCAGGACCCCAACTGTGAAATTTGTGACGACGCCCTGC 1433  
1375 |  
1376 |  
1021 QY CTCTCTGATCCCTGTCAACACAGAGGACAGCTGTGAAGGACCTCCCTGGGGCTTTGAGTGT 1080  
1022 |  
1023 |  
1434 Db CTCTCTGATCCCTGTCAACACAGAGGACAGCTGTGAAGGACCTCCCTGGGGCTTTGAGTGT 1493  
1435 |  
1436 |  
1081 QY GAGTGTTCCTCCAGGCTGACCGGGCCCACTGCTCTACAACATTTGATGACTGTTCCTCT 1140  
1082 |  
1083 |  
1494 Db GAGTGTTCCTCCAGGCTGACCGGGCCCACTGCTCTACAACATTTGATGACTGTTCCTCT 1553  
1495 |  
1496 |  
1141 QY AATAACTGTTCCTCCAGGGGCACTTGCAGGACCTGGTTAACCGATTTAAGTGTGTGTGC 1200  
1142 |  
1143 |  
1554 Db AATAACTGTTCCTCCAGGGGCACTTGCAGGACCTGGTTAACCGATTTAAGTGTGTGTGC 1613  
1555 |  
1556 |  
1201 QY CCCCCACAGTGGACTGGGAAAACGTGCCAGTTAGATGCAAAATGATGTGAGGCCAAACCT 1260  
1202 |  
1203 |  
1614 Db CCCCCACAGTGGACTGGGAAAACGTGCCAGTTAGATGCAAAATGATGTGAGGCCAAACCT 1673

1261 QY TGTGTAAACGCCAAATCTCTGTAAAGATCTCATTTGCCAGCTACTACTGCGACTGTCTTTCCC 1320  
1262 |  
1263 |  
1674 Db TGTGTAAACGCCAAATCTCTGTAAAGATCTCATTTGCCAGCTACTACTGCGACTGTCTTTCCC 1733  
1675 |  
1676 |  
1321 QY GGTGTGATGGGTGCAGAAATTTGTGACATAAATATTAATGACTGCTTGGCCAGTGTCAGAAT 1380  
1322 |  
1323 |  
1734 Db GGTGTGATGGGTGCAGAAATTTGTGACATAAATATTAATGACTGCTTGGCCAGTGTCAGAAT 1793  
1735 |  
1736 |  
1381 QY GAGCCCTCTGTGCGGATTTGGTTAATGTTATCGCTGTATCTGTCCACTGCTGCTATGCA 1440  
1382 |  
1383 |  
1794 Db GAGCCCTCTGTGCGGATTTGGTTAATGTTATCGCTGTATCTGTCCACTGCTGCTATGCA 1853  
1795 |  
1796 |  
1441 QY GCGGATCACTGTGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT 1500  
1442 |  
1443 |  
1854 Db GCGGATCACTGTGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT 1913  
1855 |  
1856 |  
1501 QY CACTGTCAAGATGAATAATCAACAGATTCAGATGAATGTGCCAGCAACCCCTGTTTCTGGAAC 1560  
1502 |  
1503 |  
1914 Db CACTGTCAAGATGAATAATCAACAGATTCAGATGAATGTGCCAGCAACCCCTGTTTCTGGAAC 1973  
1915 |  
1916 |  
1561 QY CTCCTGTCACTGAGACATCGATTAATTTCTGAGCCCTTAATCCCTGCCAGAAACGGTGCCTGCTGC 1620  
1562 |  
1563 |  
1974 Db CTCCTGTCACTGAGACATCGATTAATTTCTGAGCCCTTAATCCCTGCCAGAAACGGTGCCTGCTGC 2033  
1975 |  
1976 |  
1621 QY TACAACCGTGCCTGAGTACTATTTCTGCAAGTGCCTGAGGACTATGAGGCAAGAACTGC 1680  
1622 |  
1623 |  
2034 Db TACAACCGTGCCTGAGTACTATTTCTGCAAGTGCCTGAGGACTATGAGGCAAGAACTGC 2093  
2035 |  
2036 |  
1681 QY TCACACTGAAAGACCACTGCGCGCAGACGCCCTGTGAAAGTGAATGACAGCTGCACAGTG 1740  
1682 |  
1683 |  
2094 Db TCACACTGAAAGACCACTGCGCGCAGACGCCCTGTGAAAGTGAATGACAGCTGCACAGTG 2153  
2095 |  
2096 |  
1741 QY GCCATGGCTTCCAAACGACACACCTGAAGGGTGCCTGTATATTTCTCCAAACGCTGTGTGT 1800  
1742 |  
1743 |  
2154 Db GCCATGGCTTCCAAACGACACACCTGAAGGGTGCCTGTATATTTCTCCAAACGCTGTGTGT 2213  
2155 |  
2156 |  
1801 QY CCTCAACGGGAAGTGCAGAGTCACTGCGGAGGCAAAATTCACCTGTGACTGTGTAAACAAAGGC 1860  
1802 |  
1803 |  
2214 Db CCTCAACGGGAAGTGCAGAGTCACTGCGGAGGCAAAATTCACCTGTGACTGTGTAAACAAAGGC 2273  
2215 |  
2216 |  
1861 QY TTCAACGGGAACATACTGCGCAATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAGAAC 1920  
1862 |  
1863 |  
2274 Db TTCAACGGGAACATACTGCGCAATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAGAAC 2333  
2275 |  
2276 |  
1921 QY GGTGGCACTTGCATCCGATGGTGTCAACTCTCAAGTGCATCTGTAGTGCAGCGCTGGAG 1980  
1922 |  
1923 |  
2334 Db GGTGGCACTTGCATCCGATGGTGTCAACTCTCAAGTGCATCTGTAGTGCAGCGCTGGAG 2393  
2335 |  
2336 |  
1981 QY GGGGCCCTACTGTGAAACCAATATTAATGACTGCAGCCAGAACCCCTGCCACAATGGGGGC 2040  
1982 |  
1983 |  
2394 Db GGGGCCCTACTGTGAAACCAATATTAATGACTGCAGCCAGAACCCCTGCCACAATGGGGGC 2453  
2395 |  
2396 |  
2041 QY ACGTGTGCGAACCTGTGTCAATGACTTCTACTGTGACTGTGTAATAAATGGGTGGAAGGAAG 2100  
2042 |  
2043 |  
2454 Db ACGTGTGCGAACCTGTGTCAATGACTTCTACTGTGACTGTGTAATAAATGGGTGGAAGGAAG 2513  
2455 |  
2456 |  
2101 QY ACCCTGCCACTCAGTGCAGTGTGATGAGCCACGTCGAACACCGTGGCACCTGC 2160  
2102 |  
2103 |  
2514 Db ACCCTGCCACTCAGTGCAGTGTGATGAGCCACGTCGAACACCGTGGCACCTGC 2573  
2515 |  
2516 |  
2161 QY TATGATGAGGGGATGCTTTTAAAGTGCATGTCTCTGGCGGCTGGGAAGGAACAACTGT 2220  
2162 |  
2163 |  
2574 Db TATGATGAGGGGATGCTTTTAAAGTGCATGTCTCTGGCGGCTGGGAAGGAACAACTGT 2633  
2575 |  
2576 |  
2221 QY AACATAGCCGAAACAGTAGCTGCTGCCAAACCCCTGCCATTAATGGGGGACATGTGTG 2280  
2222 |  
2223 |  
2634 Db AACATAGCCGAAACAGTAGCTGCTGCCAAACCCCTGCCATTAATGGGGGACATGTGTG 2693  
2635 |  
2636 |  
2281 QY GTCAAACGGCGAGTCTTTTACGTGCTGCAAGGAAGGCTGGGAGGGGCCCATCTGTGCT 2340  
2282 |  
2283 |  
2694 Db GTCAAACGGCGAGTCTTTTACGTGCTGCAAGGAAGGCTGGGAGGGGCCCATCTGTGCT 2753  
2695 |  
2696 |  
2341 QY CAGAATAACCAATGACTGACGCCCTCATCCCTGTTTACAACAGCGGCACTGTGTGTGGATGGA 2400

Db 2754 CAGAAATACCAATGACTGACGACCTCATCCCTGTGTACAAACAGCGCACCTGTGTGGATGGA 2813  
Qy 2401 GACAACTGGTACCGGTGCGAATGTGCCCGGGTTTTGCTGGGCCCGACTGACAGATAAAC 2460  
Db 2814 GACAACTGGTACCGGTGCGAATGTGCCCGGGTTTTGCTGGGCCCGACTGACAGATAAAC 2873  
Qy 2461 ATCAATGAATGCCAGTCTTCACTTGTGCTTTGGAGCGACCTGTGTGGATGATCAAT 2520  
Db 2874 ATCAATGAATGCCAGTCTTCACTTGTGCTTTGGAGCGACCTGTGTGGATGATCAAT 2933  
Qy 2521 GGCTACCGGTGTGTCTGCCCTCCAGGGCACAGTGTGCTCCAAAGTCCAGGAAAGTTTCAGGG 2580  
Db 2934 GGCTACCGGTGTGTCTGCCCTCCAGGGCACAGTGTGCTCCAAAGTCCAGGAAAGTTTCAGGG 2993  
Qy 2581 AGACCTTGATCATCAGTGGGAGTGTGATACAGATGGGGCCAAATGGGATGATGACTGT 2640  
Db 2994 AGACCTTGATCATCAGTGGGAGTGTGATACAGATGGGGCCAAATGGGATGATGACTGT 3053  
Qy 2641 AATACCTGCCAGTGCCTGGAATGACGGATGCCTGTCTCAAAGTCTGTGTGGCCCTCGA 2700  
Db 3054 AATACCTGCCAGTGCCTGGAATGACGGATGCCTGTCTCAAAGTCTGTGTGGCCCTCGA 3113  
Qy 2701 CCTTGCTGCTCCACAAAGGGCACAGAGTGGCCCGAGCGGCGAGCTGCATCCCATC 2760  
Db 3114 CCTTGCTGCTCCACAAAGGGCACAGAGTGGCCCGAGCGGCGAGCTGCATCCCATC 3173  
Qy 2761 CTGGACGACAGTCTTCTGCTCCACCTGCACTGTGTGGCGGAGTGTCTGCTTCAGT 2820  
Db 3174 CTGGACGACAGTCTTCTGCTCCACCTGCACTGTGTGGCGGAGTGTCTGCTTCAGT 3233  
Qy 2821 CTCAGCGGTGAAGCAAAAGTGACCTCTGACTCTCTTATCCAGGATAACTGTGCGAAC 2880  
Db 3234 CTCAGCGGTGAAGCAAAAGTGACCTCTGACTCTCTTATCCAGGATAACTGTGCGAAC 3293  
Qy 2881 ATCACATTTACCTTTAACAGGAGATGATGTACAGGCTTTACTACGAGCACTTTGC 2940  
Db 3294 ATCACATTTACCTTTAACAGGAGATGATGTACAGGCTTTACTACGAGCACTTTGC 3353  
Qy 2941 AGTGAATTAGGAATTTGAATATTTTGAAGAAATTTTCCGCTCAATATTAATCAATCTACATC 3000  
Db 3354 AGTGAATTAGGAATTTGAATATTTTGAAGAAATTTTCCGCTCAATATTAATCAATCTACATC 3413  
Qy 3001 GCTTGGAGCTTCCCTTCAGCGAAACAATGAAATACATGTGCCCAATTTCTGTGAAGAT 3060  
Db 3414 GCTTGGAGCTTCCCTTCAGCGAAACAATGAAATACATGTGCCCAATTTCTGTGAAGAT 3473  
Qy 3061 ATACGGGATGATGGGAAACCGATCAAGGAATCACTGACAAATAATCAATCTGTGTAGT 3120  
Db 3474 ATACGGGATGATGGGAAACCGATCAAGGAATCACTGACAAATAATCAATCTGTGTAGT 3533  
Qy 3121 AAACGTGATGGAACACAGCTCGCTGATTGCTGCGGTTGCGAAGTAAGATTCAGAGCGG 3180  
Db 3534 AAACGTGATGGAACACAGCTCGCTGATTGCTGCGGTTGCGAAGTAAGATTCAGAGCGG 3593  
Qy 3181 CCTCTGAAGAACAGAACAGATTTCTTGTTCCTTGTGAGCTCTGTCTTAACTGTGGCT 3240  
Db 3594 CCTCTGAAGAACAGAACAGATTTCTTGTTCCTTGTGAGCTCTGTCTTAACTGTGGCT 3653  
Qy 3241 TGGATCTGTGTGTGTGACGGCTTCTACTGTGTGCTGCGAAGCGGCGGAGCGCGGC 3300  
Db 3654 TGGATCTGTGTGTGTGACGGCTTCTACTGTGTGCTGCGAAGCGGCGGAGCGCGGC 3713  
Qy 3301 AGCCACACACACTCAGCTCTGAGGACCAACACCAACCAACCAACCAACCAACCAACCAAC 3360  
Db 3714 AGCCACACACACTCAGCTCTGAGGACCAACACCAACCAACCAACCAACCAACCAACCAAC 3773  
Qy 3361 CAGATCAAAAACCCATTGAGAAACATGGGGCCCAACACCGTCCCTCCATCAAGGATTACGAG 3420  
Db 3774 CAGATCAAAAACCCATTGAGAAACATGGGGCCCAACACCGTCCCTCCATCAAGGATTACGAG 3833  
Qy 3421 AACAGAACTCCAAATGTCTAAATTAAGGACACAAATTTCTGAAGTAGAAGAGGACGAC 3480

Db 3834 AACAGAACTCCAAATGTCTTAAATAAGGACACACAAATCTGAAGTAGAAGAGGACGAC 3893  
Qy 3481 ATGGACAAACACACAGCAGAAAGCCCGGTTTGGCAAGCAGCGCGGTATAGCTCGTAGAC 3540  
Db 3894 ATGGACAAACACACAGCAGAAAGCCCGGTTTGGCAAGCAGCGCGGTATAGCTCGTAGAC 3953  
Qy 3541 AGAGAAG 3600  
Db 3954 AGAGAAG 4013  
Qy 3601 GACAAACAGAGACTTGGAAAGTGGCCAGAGCTTAAACCGAATGAGTACATCGTATAG 3657  
Db 4014 GACAAACAGAGACTTGGAAAGTGGCCAGAGCTTAAACCGAATGAGTACATCGTATAG 4070

RESULT 3  
US-09-566-047-1  
; Sequence 1, Application US/09566047  
; Patent No. 6703198  
; GENERAL INFORMATION:  
; APPLICANT: Li, Linheng  
; Hood, Leroy  
; Krantz, Ian D.  
; Spinner, Nancy B.  
; TITLE OF INVENTION: Methods of Diagnosing Alagille Syndrome  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/566,047  
; FILING DATE: 05-May-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/882,046  
; FILING DATE: 25-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UW 4164  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (858) 535-9001  
; TELEFAX: (858) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5590 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 414..4068  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-566-047-1

Query Match 99.9%; Score 3654.2; DB 3; Length 5590;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3653; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGCGTTCCCGGACGCGCGGTCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 60  
Db 414 ATGCGTTCCCGGACGCGCGGTCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 473

QY	61	CTCTGTGCTCGAGAGCAAGGTGTGTGGGCTCGGGTCAAGTTCAGATTGAGATCCTG	120
Db	474	CTCTGTGCTCGAGAGCAAGGTGTGTGGGCTCGGGTCAAGTTCAGATTGAGATCCTG	533
QY	121	TCCATGCGAGAACGTGAACGGGAGCTGCAGAACGGGAACCTGTCGGCGGCGCCGGAAC	180
Db	534	TCCATGCGAGAACGTGAACGGGAGCTGCAGAACGGGAACCTGTCGGCGGCGCCGGAAC	593
QY	181	CCGGGAGACCGAAGTGACCCCGGAGAGTGACATACATCTCAAGTGTGCTCAAG	240
Db	594	CCGGGAGACCGAAGTGACCCCGGAGAGTGACATACATCTCAAGTGTGCTCAAG	653
QY	241	GAGTATCAGTCCCGCTGACCGCGGGGGCCCTGACGCTTCGGCTCAGGGTCCAGCCCT	300
Db	654	GAGTATCAGTCCCGCTGACCGCGGGGGCCCTGACGCTTCGGCTCAGGGTCCAGCCCT	713
QY	301	GTATCGGGGGCAACCTTCAACCTCAAGCCGAGCGCGGCAACGCAACCGGATC	360
Db	714	GTATCGGGGGCAACCTTCAACCTCAAGCCGAGCGCGGCAACGCAACCGGATC	773
QY	361	GTGTGCTTTCAGTTCGGCTGGCGAGGTCCATATAGTGTGCTTGTGGAGGGTGGAT	420
Db	774	GTGTGCTTTCAGTTCGGCTGGCGAGGTCCATATAGTGTGCTTGTGGAGGGTGGAT	833
QY	421	TCCAGTAATGACACCGCTTCAACCTGACAGTATTATGAAAAGCTTCTCACTCGGGCATG	480
Db	834	TCCAGTAATGACACCGCTTCAACCTGACAGTATTATGAAAAGCTTCTCACTCGGGCATG	893
QY	481	ATCAACCCGAGCGGAGTGGCAGACGCTGAAGCAGAACACGGCGGTGCCCCATTGAG	540
Db	894	ATCAACCCGAGCGGAGTGGCAGACGCTGAAGCAGAACACGGCGGTGCCCCATTGAG	953
QY	541	TATCAGATCCGGTGACTGTGATGACTACTATATGGCTTTGGCTGYAATAAGTTCGC	600
Db	954	TATCAGATCCGGTGACTGTGATGACTACTATATGGCTTTGGCTGCAATAGATTCTGC	1013
QY	601	CGCCCCAGAGATGACTTCTTTGGACACTATGCCCTGACAGAAATGGCAACAAACTGC	660
Db	1014	CGCCCCAGAGATGACTTCTTTGGACACTATGCCCTGACAGAAATGGCAACAAACTGC	1073
QY	661	ATGAAGGCTGGATGGGCCCGGAATGTAACAGAGCTATTTCCGACAAAGCTCGAGTCCT	720
Db	1074	ATGAAGGCTGGATGGGCCCGGAATGTAACAGAGCTATTTCCGACAAAGCTCGAGTCCT	1133
QY	721	AAGCATGGCTTTCGAACTCCAGGTGACTGACAGGTGCCAGTGAAGCTGCAAGGCTG	780
Db	1134	AAGCATGGCTTTCGAACTCCAGGTGACTGACAGGTGCCAGTGAAGCTGCAAGGCTG	1193
QY	781	TACTGTGATAAGTGCATCCACACCCGGATGCGTCCACGGCATCTGTAATGAGCCCTGG	840
Db	1194	TACTGTGATAAGTGCATCCACACCCGGATGCGTCCACGGCATCTGTAATGAGCCCTGG	1253
QY	841	CAGTGCCTCTGTGAGACCAACTGGGGGGCGGAGCTCTGTGACAAAGATCTCAATTAAGT	900
Db	1254	CAGTGCCTCTGTGAGACCAACTGGGGGGCGGAGCTCTGTGACAAAGATCTCAATTAAGT	1313
QY	901	GGGACTCATAGCCGTGTCTCAACGGGGGAATCTGTAGCAACACAGGCCCTGACAAATAT	960
Db	1314	GGGACTCATAGCCGTGTCTCAACGGGGGAATCTGTAGCAACACAGGCCCTGACAAATAT	1373
QY	961	CAGTGTTCCTCCCTGAGGGGTATTTCAGGACCCCAACTGTGAAATTTGCTGAGCAGCCTGC	1020
Db	1374	CAGTGTTCCTCCCTGAGGGGTATTTCAGGACCCCAACTGTGAAATTTGCTGAGCAGCCTGC	1433
QY	1021	CTCTCTGATCCCTGTCAACACAGAGGCAAGCTGTGAAGGAGACCTCCCTGGGCTTTGAGTGT	1080
Db	1434	CTCTCTGATCCCTGTCAACACAGAGGCAAGCTGTGAAGGAGACCTCCCTGGGCTTTGAGTGT	1493
QY	1081	GAGTGTTCCTCCAGGCTGAGACCGGCCCCACATGCTCTACAAACATTTGATGACTGTTCTCT	1140
Db	1494	GAGTGTTCCTCCAGGCTGAGACCGGCCCCACATGCTCTACAAACATTTGATGACTGTTCTCT	1553
QY	1141	AATAACTGTTCACCGGGGACCTGCGCAGGACCTGGTTAAGCGATTAAAGTGTGTGTC	1200

Db	1554	AATAACTGTTCACCGGGGACCTGCGCAGGACCTGGTTAAACGGATTTAAGTGTGTGTGC	1613
QY	1201	CCCCACAGTGACACTGGGGAACCGTGCAGTTAGATGCAAAATGAATGTGAGGCCAAACCT	1260
Db	1614	CCCCACAGTGACACTGGGGAACCGTGCAGTTAGATGCAAAATGAATGTGAGGCCAAACCT	1673
QY	1261	TGTGTAAACGCCAAATTCCTGTAAAGATCTCATTTGCCAGCTACTACTGCGACTGTCTTCCC	1320
Db	1674	TGTGTAAACGCCAAATTCCTGTAAAGATCTCATTTGCCAGCTACTACTGCGACTGTCTTCCC	1733
QY	1321	GGCTGGAATGGGTGAGAAATTTGTCATAATAATTAATGACTGCTTGGCCAGTGTGAGAT	1380
Db	1734	GGCTGGAATGGGTGAGAAATTTGTCATAATAATTAATGACTGCTTGGCCAGTGTGAGAT	1793
QY	1381	GAGCCTCTGTCGGGATTTGGTTAATGTGTATCGCTGTATCTGTCCACTGCTATGCA	1440
Db	1794	GAGCCTCTGTCGGGATTTGGTTAATGTGTATCGCTGTATCTGTCCACTGCTATGCA	1853
QY	1441	GGCGATCACTGTGAGAGACATCCGATGAATGTGCCAGCAACCCCTGTGTAATGGGGT	1500
Db	1854	GGCGATCACTGTGAGAGACATCCGATGAATGTGCCAGCAACCCCTGTGTAATGGGGT	1913
QY	1501	CACGTGCAGAAATGAAATCAACAGATTCAGATTCAGTGTCTGTGCCACTGGTTCTCTGAAAC	1560
Db	1914	CACGTGCAGAAATGAAATCAACAGATTCAGATTCAGTGTCTGTGCCACTGGTTCTCTGAAAC	1973
QY	1561	CTCTGTGAGTGGACATCGATTTATTTGTGAGCCCTAATCCCTGCCAGAACCGTGCCAGTGC	1620
Db	1974	CTCTGTGAGTGGACATCGATTTATTTGTGAGCCCTAATCCCTGCCAGAACCGTGCCAGTGC	2033
QY	1621	TACAAACCGTGCAGTACTATTTCTGCAAGTGGCCGAGGACTATGAGGGCAAGAACTGC	1680
Db	2034	TACAAACCGTGCAGTACTATTTCTGCAAGTGGCCGAGGACTATGAGGGCAAGAACTGC	2093
QY	1681	TCACACTGAAAGACCACTGCCGACGACCCCTGTGAAAGTGAATGACAGCTGCACAGTG	1740
Db	2094	TCACACTGAAAGACCACTGCCGACGACCCCTGTGAAAGTGAATGACAGCTGCACAGTG	2153
QY	1741	GCATGGCTTCCAAACGACACACCTGAAGGGTGGGTATATTTCTCCCAACGCTGTGGT	1800
Db	2154	GCATGGCTTCCAAACGACACACCTGAAGGGTGGGTATATTTCTCCCAACGCTGTGGT	2213
QY	1801	CCTCAGGGAAAGTGAAGTCAAGTCAAGTGGGAGGCAAAATTCACCTGTGACTGTAACAAAGGC	1860
Db	2214	CCTCAGGGAAAGTGAAGTCAAGTCAAGTGGGAGGCAAAATTCACCTGTGACTGTAACAAAGGC	2273
QY	1861	TTCAACGGGAAACATACCTGCCATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAGAAC	1920
Db	2274	TTCAACGGGAAACATACCTGCCATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAGAAC	2333
QY	1921	GGTGGCACTTGCATCGATGGTCAACTCTCAAGTGCATCTGTAGTGACGGCTGGAG	1980
Db	2334	GGTGGCACTTGCATCGATGGTCAACTCTCAAGTGCATCTGTAGTGACGGCTGGAG	2393
QY	1981	GGGSCCTTACTGTGAAACCAATATTAATGACTGACGAGCAGAACCCCTGCCCAATGGGGGC	2040
Db	2394	GGGSCCTTACTGTGAAACCAATATTAATGACTGACGAGCAGAACCCCTGCCCAATGGGGGC	2453
QY	2041	ACGTGTCCGACCTGGTCAATGACTTCTACTGTGACTGTGAAATGGGTGAAAGGAAAG	2100
Db	2454	ACGTGTCCGACCTGGTCAATGACTTCTACTGTGACTGTGAAATGGGTGAAAGGAAAG	2513
QY	2101	ACCTGCCACTCAGTGCAGTGTGATGAGGCCACGTCGCAACACGGTGGCACCTGC	2160
Db	2514	ACCTGCCACTCAGTGCAGTGTGATGAGGCCACGTCGCAACACGGTGGCACCTGC	2573
QY	2161	TATGATGAGGGGATGCTTTTAAAGTGCATGTGTCTCGCGCTGGGAGGAAACACCTGT	2220
Db	2574	TATGATGAGGGGATGCTTTTAAAGTGCATGTGTCTCGCGCTGGGAGGAAACACCTGT	2633
QY	2221	AACATAGCCGAAACAGTGTGCTGCTGCCCAACCCCTGCCCATTAATGGGGGACATGTGTG	2280

Db 2634 AACATAGCCCGAAACAGTAGCTGCTGCCCAACCCCTGCCATTAATGGGGGACATGTGTG 2693  
Qy 2281 GTCAACGCGAGTCTCTTTACGTGGTCTGCAAGGAAGCTGGGAGGGCCCATCTGTGCT 2340  
Db 2694 GTCAACGCGAGTCTCTTTACGTGGTCTGCAAGGAAGCTGGGAGGGCCCATCTGTGCT 2753  
Qy 2341 CAGAAATACCAATGACTGCGAGCCCTCATCCCTGTTTACAACAGCGGACCTGTGTGGATGGA 2400  
Db 2754 CAGAAATACCAATGACTGCGAGCCCTCATCCCTGTTTACAACAGCGGACCTGTGTGGATGGA 2813  
Qy 2401 GACAACCTGTACCGGTGCGAATGTGCCCGGTTTGTGGGCGCCGACTGCGAGAAATAAC 2460  
Db 2814 GACAACCTGTACCGGTGCGAATGTGCCCGGTTTGTGGGCGCCGACTGCGAGAAATAAC 2873  
Qy 2461 ATCAATGAATGCCAGTCTTCACTTGTGCTTGGAGGACCTGTGTGGATGAGATCAAT 2520  
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Qy 2521 GGCTACCGGTGTGTCTGCCCTCCAGGGCACAGTGGTGGCAAGTCCAGGAAGTTTCAGGG 2580  
Db 2934 GGCTACCGGTGTGTCTGCCCTCCAGGGCACAGTGGTGGCAAGTCCAGGAAGTTTCAGGG 2993  
Qy 2581 AGACCTTGATCACCATGAGGAGTGTGATACAGATGGGGCCAAATGGGATGATGACTGT 2640  
Db 2994 AGACCTTGATCACCATGAGGAGTGTGATACAGATGGGGCCAAATGGGATGATGACTGT 3053  
Qy 2641 AATACCTGCCAGTCCCTGAATGGACGATGCCCTGCTCAAAGGTCTGGTGGGCCCTCGA 2700  
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Qy 2701 CCTTGCTGTCTCAAAAGGGCACAGGAGTGGCCCGGAGGAGCTGATGCCCATC 2760  
Db 3114 CCTTGCTGTCTCAAAAGGGCACAGGAGTGGCCCGGAGGAGCTGATGCCCATC 3173  
Qy 2761 CTGAGCACCAAGTCTTCTCCACCTGCACTGGTGTGGGCGAGTCTGGTCTTCAGT 2820  
Db 3174 CTGAGCACCAAGTCTTCTCCACCTGCACTGGTGTGGGCGAGTCTGGTCTTCAGT 3233  
Qy 2821 CTCAGCGGTGGAAGACAAAGTGCACCTGCTGACTCTTATACAGGATAACTGTGCGAAC 2880  
Db 3234 CTCAGCGGTGGAAGACAAAGTGCACCTGCTGACTCTTATACAGGATAACTGTGCGAAC 3293  
Qy 2881 ATCAATTTACCTTTAAACAGGAGATGATGATCAGGCTTCTACTACGGAGCAATTGTC 2940  
Db 3294 ATCAATTTACCTTTAAACAGGAGATGATGATCAGGCTTCTACTACGGAGCAATTGTC 3353  
Qy 2941 AGTGAATTTAGGAATTTGAATATTTTGAAGATGTTTCCGCTGAATATTCATCTACATC 3000  
Db 3354 AGTGAATTTAGGAATTTGAATATTTTGAAGATGTTTCCGCTGAATATTCATCTACATC 3413  
Qy 3001 GCTTGCAGGCTTCCCTTTCAGCGAACAAATGAAATACATGTGGCCATTTCTGCTGAAGAT 3060  
Db 3414 GCTTGCAGGCTTCCCTTTCAGCGAACAAATGAAATACATGTGGCCATTTCTGCTGAAGAT 3473  
Qy 3061 ATACGGGATGAGGAAACCGGATCAAGGAATCACTGACAAAATAATATTCATCTGTTAGT 3120  
Db 3474 ATACGGGATGAGGAAACCGGATCAAGGAATCACTGACAAAATAATATTCATCTGTTAGT 3533  
Qy 3121 AAACGTGATGAAACACGCTCGCTGATGTCGCTGTCGAGATGTAAGATTCAGAGCGG 3180  
Db 3534 AAACGTGATGAAACACGCTCGCTGATGTCGCTGTCGAGATGTAAGATTCAGAGCGG 3593  
Qy 3181 CCTCTGAAGAACAAACAGATTTTCTTGTTCCTTGTGCTGAGCTCTGTCTTAACTGTGGCT 3240  
Db 3594 CCTCTGAAGAACAAACAGATTTTCTTGTTCCTTGTGCTGAGCTCTGTCTTAACTGTGGCT 3653  
Qy 3241 TGAATCTGTTGTTGTTGAGCGGCTTCTAATGTTGCTGCGGAGCGGCGGAGCGCGGC 3300  
Db 3654 TGAATCTGTTGTTGTTGAGCGGCTTCTAATGTTGCTGCGGAGCGGCGGAGCGCGGC 3713  
Qy 3301 AGCCACACACCTCTGAGGACAAACCAACCAACCAACCTGCGGAGGAGCTGAAAC 3360  
Db 3714 AGCCACACACCTCTGAGGACAAACCAACCAACCAACCTGCGGAGGAGCTGAAAC 3773

Qy 3361 CAGATCAAAAACCCCATTTGAGAAACATGGGGCCAAACACGGTCCCCTCAAGGATTCAGAG 3420  
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Db 3834 AACAGAACTCCAAATGTCTAAATTAAGACACACAATTTCTGAAGTAGAAGAGGACGAC 3893  
Qy 3481 ATGGACAAACACAGACAGAAAGCCCGTTTGGCAAGCAGCGCGGTATACGCTGTTAGAC 3540  
Db 3894 ATGGACAAACACAGACAGAAAGCCCGTTTGGCAAGCAGCGCGGTATACGCTGTTAGAC 3953  
Qy 3541 AGAGAGAGAGAGGCCCCCAACCGCACCGCCGACAAAACCTGGACAAAACAAACAG 3600  
Db 3954 AGAGAGAGAGAGGCCCCCAACCGCACCGCCGACAAAACCTGGACAAAACAAACAG 4013  
Qy 3601 GACACAGAGACTTGGAAAGTCCAGAGCTTAAACCGAATGGAGTACATCGTATAG 3657  
Db 4014 GACACAGAGACTTGGAAAGTCCAGAGCTTAAACCGAATGGAGTACATCGTATAG 4070

RESULT 4  
US-09-949-016-31  
; Sequence 31, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 5896  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-31

Query Match 99.9%; Score 3654.2; DB 3; Length 5896;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3653; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATCGTTTCCCACGACRCGCGCGCGCTCGGGGCGCCCTAAGCCTCTGCTCGCCCTG 60  
Db 414 ATCGTTTCCCACGACRCGCGCGCGCTCGGGGCGCCCTAAGCCTCTGCTCGCCCTG 473  
Qy 61 CTCTGTGCTCGAGCCCAAGGTGTGTGGGCGCTCGGGTCAGTTCGAGTTGGAGATCCTG 120  
Db 474 CTCTGTGCTCGAGCCCAAGGTGTGTGGGCGCTCGGGTCAGTTCGAGTTGGAGATCCTG 533  
Qy 121 TCATTCAGAACGTGAACGGGAGCTGCAGAACCGGAACTGCTGCGGCGGCGCCGGAAC 180  
Db 534 TCATTCAGAACGTGAACGGGAGCTGCAGAACCGGAACTGCTGCGGCGGCGCCGGAAC 593  
Qy 181 CCGGAGAGCCGAAAGTGACCCCGACGAGTGTGACATACATCTTCAAAGTGTGCTCAAG 240  
Db 594 CCGGAGAGCCGAAAGTGACCCCGACGAGTGTGACATACATCTTCAAAGTGTGCTCAAG 653  
Qy 241 GAGTATCAGTCCGCGCTCAGCGCGGCGGCGCCCTGCAAGTTCGAGGTCAGGCTCCAGCCT 300  
Db 654 GAGTATCAGTCCGCGCTCAGCGCGGCGGCGCCCTGCAAGTTCGAGGTCAGGCTCCAGCCT 713  
Qy 301 GTCATCGGGGCAACACTTCAACCTCAAGGCGAGCGCGGCAACCGGCAACCGGCAATC 360



Db 714 GTCATCGGGGCAACACCTTTCAACCTCAAGGCCAGCGGCAACGACCGCAATC 773  
Qy 361 GTCTGCTTTTCACTTTTCGCTCGCCGAGTCCCTATACGTTGCTTGTGGAGGCTGGGAT 420  
Db 774 GTCTGCTTTTCACTTTTCGCTCGCCGAGTCCCTATACGTTGCTTGTGGAGGCTGGGAT 833  
Qy 421 TCCAGTAATGACACCGTTCAACCTGACAGTATTATTGAAAAGGCTTCTCACTCGGCGATG 480  
Db 834 TCCAGTAATGACACCGTTCAACCTGACAGTATTATTGAAAAGGCTTCTCACTCGGCGATG 893  
Qy 481 ATCAACCCGAGCGGAGTGGCAGAGCGCTGAAGCAGAACACGCGGCTGTGCCACTTTGAG 540  
Db 894 ATCAACCCGAGCGGAGTGGCAGAGCGCTGAAGCAGAACACGCGGCTGTGCCACTTTGAG 953  
Qy 541 TATCAGATCCGCTGACCTGTGATGACTACTACTATAGGCTTTGGCTGYAATAAGTTCTGC 600  
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Qy 601 CGCCCCAGAGATGACTTCTTTTGGACACTATGCCCTGTGACAGAAATGGCAACAAACTTGC 660  
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Qy 661 ATGGAAGGCTGGATGGGCCCGCAATGTAACAGAGCTATTGGCCGACAAAGCTCGAGTCCT 720  
Db 1074 ATGGAAGGCTGGATGGGCCCGCAATGTAACAGAGCTATTGGCCGACAAAGCTCGAGTCCT 1133  
Qy 721 AAGCATGGGCTTGTCAAACTCCAGGTGACTGCGAGGTGCCAGTAYGGCTGGCAAGGCTTG 780  
Db 1134 AAGCATGGGCTTGTCAAACTCCAGGTGACTGCGAGGTGCCAGTAYGGCTGGCAAGGCTTG 1193  
Qy 781 TACTGTGATAAGTGCATCCACACCCCGGATGCGTCCACGGCATCTGTAATGAGCCCTGG 840  
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Qy 841 CAGTGCCTCTGTGAGACCAACTGGGGCGGCAGCTCTGTGACAAAAGATCTCAATTAAGTGT 900  
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Db 1314 GGGACTCATCAGCCGCTGTCTCAAGGGGGAACCTGTGAGCAACACAGGCCCTGCAAAATAT 1373  
Qy 961 CAGTGTTCCTGCCCTGAGGGGTATTCAAGGACCCCAACTGTGAAATGTGTGAGCAGCCCTGC 1020  
Db 1374 CAGTGTTCCTGCCCTGAGGGGTATTCAAGACCCCAACTGTGAAATGTGTGAGCAGCCCTGC 1433  
Qy 1021 CTCTCTGATCCCTGTCAACACAGAGGCGAGCTGTGAAGGAGACCTCCCTGGGCTTTGAGTGT 1080  
Db 1434 CTCTCTGATCCCTGTCAACACAGAGGCGAGCTGTGAAGGAGACCTCCCTGGGCTTTGAGTGT 1493  
Qy 1081 GAGTGTTCCTGAGCTGGACCGGCCCCACATGCTCTACAAACATTTGATGACTGTTCTCCT 1140  
Db 1494 GAGTGTTCCTGAGCTGGACCGGCCCCACATGCTCTACAAACATTTGATGACTGTTCTCCT 1553  
Qy 1141 AATAACTGTTCCACGGGGGCACTGCGCAGGACCTGGTTAACGGATTTAAAGTGTGTGTCG 1200  
Db 1554 AATAACTGTTCCACGGGGGCACTGCGCAGGACCTGGTTAACGGATTTAAAGTGTGTGTCG 1613  
Qy 1201 CCCCCACAGTGGACTGGGAAAACGTGCGAGTGTAGATGCAATGAATGTGAGGCGCAAACT 1260  
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Qy 1261 TGTGTAAACGGCAATCCTGTGAAGATCTCAATTCGCGAGCTACTACTCGGCTGCTTCCC 1320  
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Qy 1321 GGCTTGGATGGGTGAGAAATTTGTGACATAAATTAATGACTCCCTTGGCCAGTGTGAGAAT 1380  
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Qy 1441 GGCGATCACTGTGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGT 1500  
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Db 1914 CACTGTGAGAAATCAACAGATTCAGTGTCTGTGTGCCACTGTTTCTCTGGAAC 1973  
Qy 1561 CTCTGTCACTGGACATCGATTTATTGTGAGCTTATCCCTGCCAGAACCGTGCCTAGTGC 1620  
Db 1974 CTCTGTCACTGGACATCGATTTATTGTGAGCTTATCCCTGCCAGAACCGTGCCTAGTGC 2033  
Qy 1621 TACAACCGTGCAGTCACTATTCTCAAGTGTCCCGAGGACTATCAGGGCAAGAACTGC 1680  
Db 2034 TACAACCGTGCAGTCACTATTCTTCAAGTGTCCCGAGGACTATCAGGGCAAGAACTGC 2093  
Qy 1681 TCACACTGAAAGACCACTGCCGACGACCCCTGTGAAAGTGTGACAGCTGCACAGTG 1740  
Db 2094 TCACACTGAAAGACCACTGCCGACGACCCCTGTGAAAGTGTGACAGCTGCACAGTG 2153  
Qy 1741 GCCATGGCTTCCNACGACACACTGGAAGGTGCGGTATATTTCTCCCAACGTCCTGTGT 1800  
Db 2154 GCCATGGCTTCCNACGACACACTGGAAGGTGCGGTATATTTCTCCCAACGTCCTGTGT 2213  
Qy 1801 CCTCACGGGAAGTCAAGAGTCACTCGGAGGCAAAATTACCTGTGTGATGTGTAAACAAAGGC 1860  
Db 2214 CCTCACGGGAAGTCAAGAGTCACTCGGAGGCAAAATTACCTGTGTGATGTGTAAACAAAGGC 2273  
Qy 1861 TTCACGGGAACATPACTGCCAATATTAATGACTGTGAGAGCAACCCCTGTGTAGAAC 1920  
Db 2274 TTCACGGGAACATPACTGCCAATATTAATGACTGTGAGAGCAACCCCTGTGTAGAAC 2333  
Qy 1921 GGTGGCACTTGCATCGATGGTGTCACTCTACAAGTGCATCTGTAGTGACGCTGGAG 1980  
Db 2334 GGTGGCACTTGCATCGATGGTGTCACTCTACAAGTGCATCTGTAGTGACGCTGGAG 2393  
Qy 1981 GGGGCTTACTGTGAAAACCAATATTAATGACTGACGACAGCAACCCCTGCCCAAAATGGGGGC 2040  
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Qy 2041 ACCTGTGCGGACCTGTGTCAATGACTTCTACTGTGACTGTGTAATAATGGGTGGAAAG 2100  
Db 2454 ACCTGTGCGGACCTGTGTCAATGACTTCTACTGTGACTGTGTAATAATGGGTGGAAAG 2513  
Qy 2101 ACCTGCCACTCACTGACAGTGTGTGAGGCAACGTCGACCAACCGTGCACCTGC 2160  
Db 2514 ACCTGCCACTCACTGACAGTGTGTGAGGCAACGTCGACCAACCGTGCACCTGC 2573  
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Db 2574 TATGATGAGGGGATGCTTTTAAAGTGCATGTGTCTTGGCGGCTGGGAAGGAAACCACTGT 2633  
Qy 2221 AACATAGCCGAAACAGTGTGCTGCCCAACCCCTGCCATTAATGGGGGCAATGTGTG 2280  
Db 2634 AACATAGCCGAAACAGTGTGCTGCCCAACCCCTGCCATTAATGGGGGCAATGTGTG 2693  
Qy 2281 GTCAACGGCGAGTCTTTACGTGGTCTCAAGGAGGCTGGGAGGGGCCCATCTGTGCT 2340  
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US-09-949-016-4426  
; Sequence 4426, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4426  
; LENGTH: 5885  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-4426  
  
Query Match 99.9%; Score 3651; DB 3; Length 5885;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3651; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
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QY	961	CAGTGTCTGCCCTGAGGGGTATTTAGGACCCAACTGTGTGAATTTGTGTAGGACCGCTGC	1020
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QY	1021	CTCTCTGATCCCTGTGACACAGAGGAGCTGTAAAGGAGACCTCCCTGGCTTTTGAGTGT	1080
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QY	2581	AGACCTTGATCACCATGGGGAGTGTATACAGATGGGGCCAAATGGGATGATGACTGT	2640
Db	2993	AGACCTTGATCACCATGGGGAGTGTATACAGATGGGGCCAAATGGGATGATGACTGT	3052
QY	2641	AATACCTGCGCAGTCCCTGAATGACCGGATCGCCTGTCTCAAGGTCTGTGTGGCCCTCGA	2700
Db	3053	AATACCTGCGCAGTCCCTGAATGACCGGATCGCCTGTCTCAAGGTCTGTGTGGCCCTCGA	3112
QY	2701	CCTTGCTGTCTCAAAAGGGCACAGGAGTGTGCCACGCGGGCAGAGCTGCATCCCCATC	2760
Db	3113	CCTTGCTGTCTCAAAAGGGCACAGGAGTGTGCCACGCGGGCAGAGCTGCATCCCCATC	3172
QY	2761	CTGAGCAGACAGTCTGTCTGCGCCCTGACCTGTGTGGGGCAGTGTCTGTCTTCAGT	2820
Db	3173	CTGAGCAGACAGTCTGTCTGCGCCCTGACCTGTGTGGGGCAGTGTCTGTCTTCAGT	3232
QY	2821	CTCAGCGCGTGAAGACAAAGTGCACCTCTGACTCTCTATTACAGGATAAATCTGTGCGAAC	2880
Db	3233	CTCAGCGCGTGAAGACAAAGTGCACCTCTGACTCTCTATTACAGGATAAATCTGTGCGAAC	3292
QY	2881	ATCACATTTACTTTAAACAGGAGATGATGTACACGAGTCTTACTACGGAGCAATTTTC	2940
Db	3293	ATCACATTTACTTTAAACAGGAGATGATGTACACGAGTCTTACTACGGAGCAATTTTC	3352
QY	2941	AGTGAATTTGAGGAATTTTGAATAATTTTGAAGAAATTTTCCCGCTGAATTTCAATCTACATC	3000
Db	3353	AGTGAATTTGAGGAATTTTGAATAATTTTGAAGAAATTTTCCCGCTGAATTTCAATCTACATC	3412
QY	3001	GCTTTCGAGGCTTCCCTTCAGCGAAACAAATGATGTGGCCATTTTCTGTGGAAGAT	3060

[illegible]

## RESULT 7

RESOUR. 1  
 US-09-917-254-34  
 ; Patent 34, Application US/09917254  
 ; Sequence No. 6703204  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mutter, George  
 ; APPLICANT: Baak, Jan  
 ; TITLE OF INVENTION: Prognostic Classification of Breast Cancer  
 ; FILE REFERENCE: B0801/7224(JRV)  
 ; CURRENT APPLICATION NUMBER: US/09/917,254  
 ; CURRENT FILING DATE: 2001-07-27  
 ; PRIOR APPLICATION NUMBER: US 60/222,093  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 102  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 34  
 ; LENGTH: 4855  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-09-917-254-34

Query Match	99.8%	Score 3649.4	DB 3	Length 4855
Best Local Similarity	99.8%	Pred. No. 0		
Matches 3650	Conservative	3	Mismatches 4	Indels 0
			Gaps 0	
Qy	1	ATCGGTTCCACAGGACRCGCGCCGCGTCGCGGCGCCCTTAAGCCTCTCTGTCGCGCCTG	60	
Db	371	ATCGGTTCCACAGGACACAGCGCCGCGTCGCGGCGCCCTTAAGCCTCTCTGTCGCGCCTG	430	

Qy	61	CTCTGTGCCCTCGGAGCGAAAGTGTGTGGGGCCCTCGGGTCAGTTTCGAGTTGGAGATCCTG	120
Db	431	CTCTGTGCCCTCGGAGCGAAAGTGTGTGGGGCCCTCGGGTCAGTTTCGAGTTGGAGATCCTG	490
Qy	121	TCCATGTCAGAACTGAACGGGGAGCTGCAGAACGGGAACCTGCTCGGCGGGCCCGGAAC	180
Db	491	TCCATGTCAGAACTGAACGGGGAGCTGCAGAACGGGAACCTGCTCGGCGGGCCCGGAAC	550
Qy	181	CCGGGAGACCGCAAGTGCACCCGCGACGAGTGTGCACATACCTTCAAAGTGTGCCTCAAG	240
Db	551	CCGGGAGACCGCAAGTGCACCCGCGACGAGTGTGCACATACCTTCAAAGTGTGCCTCAAG	610
Qy	241	GAGTATCAGTCCCGGTCACGGCCGGGGGCCCTCGAGCTTCGGCTCAGGGTCCACGCCCT	300
Db	611	GAGTATCAGTCCCGGTCACGGCCGGGGGCCCTCGAGCTTCGGCTCAGGGTCCACGCCCT	670
Qy	301	GTCAATCGGGGGCAACACTTCAACCTCAAGCCAGCCGCGCAACGACCAACCCGATC	360
Db	671	GTCAATCGGGGGCAACACTTCAACCTCAAGCCAGCCGCGCAACGACCAACCCGATC	730
Qy	361	GTGCTGCTTTTCAGTTTTCGCTCGGCCGAGTCCCTATACCTTGTGTGTGGAGGGTGGGAT	420
Db	731	GTGCTGCTTTTCAGTTTTCGCTCGGCCGAGTCCCTATACCTTGTGTGTGGAGGGTGGGAT	790
Qy	421	TCCAGTAAATGACACCGTTTCAACCTGACAGTATTATTGAAAAGGCTTCTCACTCGGGCATG	480
Db	791	TCCAGTAAATGACACCGTTTCAACCTGACAGTATTATTGAAAAGGCTTCTCACTCGGGCATG	850
Qy	481	ATCAACCCAGCCGCGAGTGGCAGACGCTGACAGCAACACGGCGTTGCCACTTTGAG	540
Db	851	ATCAACCCAGCCGCGAGTGGCAGACGCTGACAGCAACACGGCGTTGCCACTTTGAG	910
Qy	541	TATCAGATCCGCTGACCTGTGATGACTACTACTATGGCTTTGGCTGYAATAAGTTCTCGC	600
Db	911	TATCAGATCCGCTGACCTGTGATGACTACTACTATGGCTTTGGCTGYAATAAGTTCTCGC	970
Qy	601	CGCCCCAGAGATGACTTTCTTTTGGACACTATGCTCTGTGACAGAAATGSCAACAACTTGC	660
Db	971	CGCCCCAGAGATGACTTTCTTTTGGACACTATGCTCTGTGACAGAAATGSCAACAACTTGC	1030
Qy	661	ATGGAAAGCTGGATGGGCCCCGAAATGTACAGAGACTATTTGCCGCAAGAGCTGCAGTCT	720
Db	1031	ATGGAAAGCTGGATGGGCCCCGAAATGTACAGAGACTATTTGCCGCAAGAGCTGCAGTCT	1090
Qy	721	AAGCATGGGTCTTTGCAAACTCCAGGTGACTGCGAGTGCCAGTAYAGCTGGCAAGGCCCTG	780
Db	1091	AAGCATGGGTCTTTGCAAACTCCAGGTGACTGCGAGTGCCAGTAYAGCTGGCAAGGCCCTG	1150
Qy	781	TACTGTGATAAGTGCAATCCACACCCGGGATCGGTCCACGGCATCTGTAAATGAGCCCTGG	840
Db	1151	TACTGTGATAAGTGCAATCCACACCCGGGATCGGTCCACGGCATCTGTAAATGAGCCCTGG	1210
Qy	841	CAGTGCCTCTGTGAGACCAACTGGGGGGCCAGCTCTGTGACAAAGATCTCAATTACTGT	900
Db	1211	CAGTGCCTCTGTGAGACCAACTGGGGGGCCAGCTCTGTGACAAAGATCTCAATTACTGT	1270
Qy	901	GGGACTCATCAGCCGTGTCTCAACGGGGGAACTTTGTAGCAACACAGGCCCTGCAAAATAT	960
Db	1271	GGGACTCATCAGCCGTGTCTCAACGGGGGAACTTTGTAGCAACACAGGCCCTGCAAAATAT	1330
Qy	961	CAGTGTTCCTGCTGAGGGGTATTCAAGACCCAACTGTGTAATAATGCTGAGCAGCCTGC	1020
Db	1331	CAGTGTTCCTGCTGAGGGGTATTCAAGACCCAACTGTGTAATAATGCTGAGCAGCCTGC	1390
Qy	1021	CTCTCTGATCCCTGTCAACACAGGCGAGTGTAAAGGAGCCTCCCTGGGCTTTGAGTGT	1080
Db	1391	CTCTCTGATCCCTGTCAACACAGGCGAGTGTAAAGGAGCCTCCCTGGGCTTTGAGTGT	1450
Qy	1081	GAGTGTTCCTGAGGCTGGACCGGCCCCACATGCTCTACAAACATTTGATGACTGTTCTCCT	1140
Db	1451	GAGTGTTCCTGAGGCTGGACCGGCCCCACATGCTCTACAAACATTTGATGACTGTTCTCCT	1510
Qy	1141	AATAACTGTTTCCACCGGGGSCACTCTGCCGAGACCTGGTTAACGGATTTAAGTGTGTGTGC	1200

Db	1511	 AATAACTGTTCCCAACGGGGCACCCTGCAGGACCTGGTTAAACGGATTTAAGTGTGTGTGC	1570
Qy	1201	CCCCCAGCTGGACTGGGAAAACTGGCCAGTTAGATGCAAAATGAATGTGTAGGGCCAAACCT	1260
Db	1571	CCCCCAGCTGGACTGGGAAAACTGGCCAGTTAGATGCAAAATGAATGTGTAGGGCCAAACCT	1630
Qy	1261	TGTGTAAACGCCAAATCCTGTAAAGAACTCTCATTTGCCAGCTACTACTGCAGCTGTCTTCCC	1320
Db	1631	TGTGTAAACGCCAAATCCTGTAAAGAACTCTCATTTGCCAGCTACTACTGCAGCTGTCTTCCC	1690
Qy	1321	GGCTGGATGGGTGAGAAATTTGTGACATATAATTAATGACTGGCCTTGGCCAGTGTCAGAAT	1380
Db	1691	GGCTGGATGGGTGAGAAATTTGTGACATATAATTAATGACTGGCCTTGGCCAGTGTCAGAAT	1750
Qy	1381	GACCCCTCTCTCGGGATTTGGTTAAATGGTTATCGCTGTATCTGTCCACTCGCTCATGCA	1440
Db	1751	GACCCCTCTCTCGGGATTTGGTTAAATGGTTATCGCTGTATCTGTCCACTCGCTCATGCA	1810
Qy	1441	GGCGATCACTGTGAGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT	1500
Db	1811	GGCGATCACTGTGAGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT	1870
Qy	1501	CACCTGTGAGAAATGAACAGAAATCCAGTGTCTGTGTCCCACTGGTTTTCTCTGGAAC	1560
Db	1871	CACCTGTGAGAAATGAACAGAAATCCAGTGTCTGTGTCCCACTGGTTTTCTCTGGAAC	1930
Qy	1561	CTCTGTGAGCTGGACATCGATTAATGTGAGCCTTAATCCCTGCCAGAACGGTCCCACTGC	1620
Db	1931	CTCTGTGAGCTGGACATCGATTAATGTGAGCCTTAATCCCTGCCAGAACGGTCCCACTGC	1990
Qy	1621	TACAACCGTGGCAGTGACTATTTCTGCAAGTGCCCGCAGGACTATGAGGSCAAGAACTGC	1680
Db	1991	TACAACCGTGGCAGTGACTATTTCTGCAAGTGCCCGCAGGACTATGAGGSCAAGAACTGC	2050
Qy	1681	TCACACCTGAAAGACCACTGCCGACGACCCCTGTGCAAGTGATGACAGCTGCACAGTG	1740
Db	2051	TCACACCTGAAAGACCACTGCCGACGACCCCTGTGCAAGTGATGACAGCTGCACAGTG	2110
Qy	1741	GCCATGGCTTCCAACGACACACCTGGAAGGGTGGGTATATTTCTTCCAAGCTGTGGT	1800
Db	2111	GCCATGGCTTCCAACGACACACCTGGAAGGGTGGGTATATTTCTTCCAAGCTGTGGT	2170
Qy	1801	CCTCACGGGAAGTGCAGAGTCACTGCGGAGGCAAAATTCACCTGTGTACTGTAAACAAGGC	1860
Db	2171	CCTCACGGGAAGTGCAGAGTCACTGCGGAGGCAAAATTCACCTGTGTACTGTAAACAAGGC	2230
Qy	1861	TTACACGGGAACATATGCCATGAAAAATTTAATGACTGTGAGAGCAACCTTGTAGAAAC	1920
Db	2231	TTACACGGGAACATATGCCATGAAAAATTTAATGACTGTGAGAGCAACCTTGTAGAAAC	2290
Qy	1921	GGTGGCACTTCGATCGATGGTGTCACTCCTACAAGTGCATCTGTAGTACGGCTGGGAG	1980
Db	2291	GGTGGCACTTCGATCGATGGTGTCACTCCTACAAGTGCATCTGTAGTACGGCTGGGAG	2350
Qy	1981	GGGGCTACTGTGAAAAACCAATTAATGACTGCAGCCAGAACCCCTGCACAAATGGGGGC	2040
Db	2351	GGGGCTACTGTGAAAAACCAATTAATGACTGCAGCCAGAACCCCTGCACAAATGGGGGC	2410
Qy	2041	ACGTGTCCGCACTGGTCAATGACTTCTACTGTGACTGTAAAAATGGGTGGAAGGAAAG	2100
Db	2411	ACGTGTCCGCACTGGTCAATGACTTCTACTGTGACTGTAAAAATGGGTGGAAGGAAAG	2470
Qy	2101	ACCTGCCACTCACGTGACAGTCACTGTGATGATGAGGCCAGTGCACACGGTGGCACCTGC	2160
Db	2471	ACCTGCCACTCACGTGACAGTCACTGTGATGATGAGGCCAGTGCACACGGTGGCACCTGC	2530
Qy	2161	TATGATGAGGGGATGCTTTTAAAGTGCAATGTCTCTGGCGCTCGGAAGGAAACCACTGT	2220
Db	2531	TATGATGAGGGGATGCTTTTAAAGTGCAATGTCTCTGGCGCTCGGAAGGAAACCACTGT	2590
Qy	2221	AACATAGCCGAAAAACAGTAGCTGCTGCCCAACCCCTGCCATAATATGGGGGCACATGTGT	2280

2591	Db	AA	CAT	TAC	CGG	AAA	CAG	TAG	CTG	CTG	CC	CA	CC	CTG	CC	CA	CC	CTG	CC	CA	TAA	TGG	GG	CG	CA	TG	TG	G	2655		
2281	Qy	GT	CAA	CGG	CG	AG	T	CT	TTT	TAC	TG	TG	CG	T	CTG	CA	AG	GA	AG	GT	TG	GA	G	GG	G	CC	CA	T	CTG	G	2340
2651	Db	GT	CAA	CGG	CG	AG	T	CT	TTT	TAC	TG	TG	CG	T	CTG	CA	AG	GA	AG	GT	TG	GA	G	GG	G	CC	CA	T	CTG	G	2710
2341	Qy	CAG	AAT	AC	CA	TG	CA	CTG	CAG	CC	CT	CA	T	CC	T	GT	T	CA	A	CAG	CGG	CA	CT	TG	TG	TG	G	GA	TG	G	2400
2711	Db	CAG	AAT	AC	CA	TG	CA	CTG	CAG	CC	CT	CA	T	CC	T	GT	T	CA	A	CAG	CGG	CA	CT	TG	TG	TG	G	GA	TG	G	2770
2401	Qy	GAC	AA	CTG	TAC	CGG	TG	CG	GA	TG	TG	CC	CG	GG	T	TT	TG	TG	GG	CC	CG	AC	TG	CG	CA	GA	AA	AA	C	2460	
2771	Db	GAC	AA	CTG	TAC	CGG	TG	CG	GA	TG	TG	CC	CG	GG	T	TT	TG	TG	GG	CC	CG	AC	TG	CG	CA	GA	AA	AA	C	2830	
2461	Qy	AT	CA	AT	GA	AT	GC	CT	T	TG	CG	CT	T	TG	CG	AG	CG	AC	CT	TG	TG	GA	TG	GA	TG	CA	AT	2520			
2831	Db	AT	CA	AT	GA	AT	GC	CT	T	TG	CG	CT	T	TG	CG	AG	CG	AC	CT	TG	TG	GA	TG	GA	TG	CA	AT	2890			
2521	Qy	GG	TA	CCG	TG	TG	CT	TG	CC	CT	CAG	GG	CA	CAG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	2580
2891	Db	GG	TA	CCG	TG	TG	CT	TG	CC	CT	CAG	GG	CA	CAG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	2950
2581	Qy	AG	AC	CT	TG	CA	T	CA	CT	TG	GG	AG	TG	T	GA	T	CA	CAG	AT	TG	GG	CC	AA	A	TG	GA	TG	AT	GA	CT	2640
2951	Db	AG	AC	CT	TG	CA	T	CA	CT	TG	GG	AG	TG	T	GA	T	CA	CAG	AT	TG	GG	CC	AA	A	TG	GA	TG	AT	GA	CT	3010
2641	Qy	AA	TAC	CT	GC	CA	GT	CC	TG	AA	TG	CA	CG	AT	CG	CT	TG	CT	CA	AA	GG	T	CT	TG	TG	TG	TG	CC	CT	CG	2700
3011	Db	AA	TAC	CT	GC	CA	GT	CC	TG	AA	TG	CA	CG	AT	CG	CT	TG	CT	CA	AA	GG	T	CT	TG	TG	TG	TG	CC	CT	CG	3070
2701	Qy	CT	TG	CC	TG	CT	CA	AA	AG	GG	CA	CAG	GA	TG	CC	CA	CAG	GG	GG	CA	GA	CT	GC	AT	CC	CC	CA	T	2760		
3071	Db	CT	TG	CC	TG	CT	CA	AA	AG	GG	CA	CAG	GA	TG	CC	CA	CAG	GG	GG	CA	GA	CT	GC	AT	CC	CC	CA	T	3130		
2761	Qy	CT	GA	CG	AC	AG	TG	CT	CG	T	CA	CC	CT	GC	AC	T	CT	GA	CT	TG	GG	CG	AG	TG	CT	CG	CT	CC	AG	2820	
3131	Db	CT	GA	CG	AC	AG	TG	CT	CG	T	CA	CC	CT	GC	AC	T	CT	GA	CT	TG	GG	CG	AG	TG	CT	CG	CT	CC	AG	3190	
2821	Qy	CT	CA	G	CC	GG	TG	GA	AG	CA	AA	AG	TG	CA	CT	CT	GA	CT	CT	TAT	TAC	CA	GGA	TAA	CT	TG	CG	CA	AC	2880	
3191	Db	CT	CA	G	CC	GG	TG	GA	AG	CA	AA	AG	TG	CA	CT	CT	GA	CT	CT	TAT	TAC	CA	GGA	TAA	CT	TG	CG	CA	AC	3250	
2881	Qy	AT	CA	CAT	T	TAC	TTT	AA	CA	AG	G	A	TG	AT	GT	CA	CC	AG	GT	CT	T	ACT	AC	GG	AG	CA	CAT	T	TGC	2940	
3251	Db	AT	CA	CAT	T	TAC	TTT	AA	CA	AG	G	A	TG	AT	GT	CA	CC	AG	GT	CT	T	ACT	AC	GG	AG	CA	CAT	T	TGC	3310	
2941	Qy	AG	TGA	TT	GAG	GA	TTT	TGA	TAT	TTT	TGA	GA	TTT	TCC	G	CT	G	GA	TAT	T	CA	A	T	CT	CA	AT	C	T	C	3000	
3311	Db	AG	TGA	TT	GAG	GA	TTT	TGA	TAT	TTT	TGA	GA	TTT	TCC	G	CT	G	GA	TAT	T	CA	A	T	CT	CA	AT	C	T	C	3370	
3001	Qy	G	CTT	G	CG	AG	C	T	T	C	C	C	T	T	C	CA	G	GA	CA	A	T	G	A	A	T	A	T	A	T	G	3060
3371	Db	G	CTT	G	CG	AG	C	T	T	C	C	C	T	T	C	CA	G	GA	CA	A	T	G	A	A	T	A	T	A	T	G	3430
3061	Qy	AT	AC	G	G	AT	G	A	T	G	G	AA	T	CA	CT	CA	G	AA	A	T	A	A	T	AA	T	AA	T	AA	T	AA	3120
3431	Db	AT	AC	G	G	AT	G	A	T	G	G	AA	T	CA	CT	CA	G	AA	A	T	A	A	T	AA	T	AA	T	AA	T	AA	3490
3121	Qy	AA	AC	T	GA	AG	AA	C	AG	CT	T	G	CG	GG	T	G	CG	GG	T	G	CG	GG	T	G	CG	GG	T	G	CG	GG	3180
3491	Db	AA	AC	T	GA	AG	AA	C	AG	CT	T	G	CG	GG	T	G	CG	GG	T	G	CG	GG	T	G	CG	GG	T	G	CG	GG	3550
3181	Qy	C	CT	T	G	A	A	G	A	A	C	A	G	A	T	T	C	T	T	G	T	T	C	C	T	T	C	T	T	G	3240
3351	Db	C	CT	T	G	A	A	G	A	A	C	A	G	A	T	T	C	T	T	G	T	T	C	C	T	T	C	T	T	G	3610
3241	Qy	T	G	G	A	T	C	T	T	G	T	G	A	C	G	G	C	T	T	C	T	A	C	T	G	T	G	T	G	A	3300
3611	Db	T	G	G	A	T	C	T	T	G	T	G	A	C	G	G	C	T	T	C	T	A	C	T	G	T	G	T	G	A	3670
3301	Qy	A	G	C	A	C	A	C	A	C	T	G	A	G	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C	3360
3671	Db	A	G	C	A	C	A	C	A	C	T	G	A	G	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C	3730









Qy 3601 GACACAGAGACTTGGAAAGTCCAGAGCTTAAACCGAATGAGTACATCGTATAG 3657  
Db 4009 GACAAAGAGACTTGGAAAGTCCAGAGCTTAAACCGAATGAGTACATCGTATAG 4065

RESULT 9

US-09-855-722-6  
; Sequence 6, Application US/09855722  
; Patent No. 6638741  
; GENERAL INFORMATION:  
; APPLICANT: Sakano, Seiji  
; APPLICANT: Itoh, Akira  
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE  
; FILE REFERENCE: KP-8576  
; CURRENT APPLICATION NUMBER: US/09/855,722  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/214,278  
; PRIOR FILING DATE: 1999-01-26  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 4208  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (409)..(4062)  
; NAME/KEY: sig\_peptide  
; LOCATION: (409)..(501)  
; NAME/KEY: mat\_peptide  
; LOCATION: (502)..(4062)  
US-09-855-722-6

Query Match 99.8%; Score 3647.8; DB 3; Length 4208;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3649; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGCGTTCCACGACRCCGCGCGCTCCGGGCGCCCCCTAAGCCTCTGCTCGCCCTG 60  
Db 409 ATGCGTTCCACGACGCGCGCGCTCCGGGCGCCCCCTAAGCCTCTGCTCGCCCTG 468  
Qy 61 CTCTGTGCTCCGAGCCAGAGTGTGTGGGCGCTCGGCTCAGTTGAGTGGAGTCTTG 120  
Db 469 CTCTGTGCTCCGAGCCAGAGTGTGTGGGCGCTCGGCTCAGTTGAGTGGAGTCTTG 528  
Qy 121 TCCATGACAGACGTTGAACCGGAGCTGCAGAACGGGAACTGCTGCGGCGCGCCGGAAC 180  
Db 529 TCCATGACAGACGTTGAACCGGAGCTGCAGAACGGGAACTGCTGCGGCGCGCCGGAAC 588  
Qy 181 CCGGAGACCGCAAGTGCACCCGCGACGAGTGTGACACATCTTCAAAGTGTGCTCAAG 240  
Db 589 CCGGAGACCGCAAGTGCACCCGCGACGAGTGTGACACATCTTCAAAGTGTGCTCAAG 648  
Qy 241 GAGTATCAGTCCCGCTGACGCGCGGCGGCGCTCGAGCTTCGGCTCAGGGTCCAGCCT 300  
Db 649 GAGTATCAGTCCCGCTGACGCGCGGCGGCGCTCGAGCTTCGGCTCAGGGTCCAGCCT 708  
Qy 301 GTCATCGGGGGCAACACTTCAACCTCAAGCCAGCGCGCGGCAACGACCGCAACCGCATC 360  
Db 709 GTCATCGGGGGCAACACTTCAACCTCAAGCCAGCGCGCGGCAACGACCGCAACCGCATC 768  
Qy 361 GTGCTGCTTTTCAAGTTTCGCTGCGCGAGGTCTCTATACGTTGCTTGTGGAGCGGTGGAT 420  
Db 769 GTGCTGCTTTTCAAGTTTCGCTGCGCGAGGTCTCTATACGTTGCTTGTGGAGCGGTGGAT 828  
Qy 421 TCCAGTAATGACACCGTTCAACCTGACAGTATTTATGAAAGGCTTCTCATCTGGGCGATG 480  
Db 829 TCCAGTAATGACACCGTTCAACCTGACAGTATTTATGAAAGGCTTCTCATCTGGGCGATG 888  
Qy 481 ATCAACCCGACCGGAGTGGAGAGCGCTCAAGCAGAACACGCGCGTTCGCCACTTTTGG 540  
Db 889 ATCAACCCGACCGGAGTGGAGAGCGCTCAAGCAGAACACGCGCGTTCGCCACTTTTGG 948

Qy 541 TATCAGATCCGCTGACCTGTGATGACTACTATATGGCTTTGGCTGYAATAAGTTCTGC 600  
Db 949 TATCAGATCCGCTGACCTGTGATGACTACTATATGGCTTTGGCTGYAATAAGTTCTGC 1008  
Qy 601 CGCCCCAGAGATGACTTTCTTTGGACACTATGCTGTGACAGATGCGATGCGACAAACTTGC 660  
Db 1009 CGCCCCAGAGATGACTTTCTTTGGACACTATGCTGTGACAGATGCGATGCGACAAACTTGC 1068  
Qy 661 ATGGAAGGCTGGATGGGCCCCGGAATGTAAACAGAGCTATTTGCCGACAAAGGCTGCAGTCT 720  
Db 1069 ATGGAAGGCTGGATGGGCCCCGGAATGTAAACAGAGCTATTTGCCGACAAAGGCTGCAGTCT 1128  
Qy 721 AAGCATGGGCTTTGCAAACTCCAGAGTACTGCGAGTGCAGTAYGGCTGGCAAGGCTG 780  
Db 1129 AAGCATGGGCTTTGCAAACTCCAGAGTACTGCGAGTGCAGTAYGGCTGGCAAGGCTG 1188  
Qy 781 TACTGTGATAAGTGCATCCACACCCGGGATGCTGACGGGCTGCTGTAATGAGCCCTGG 840  
Db 1189 TACTGTGATAAGTGCATCCACACCCGGGATGCTGACGGGCTGCTGTAATGAGCCCTGG 1248  
Qy 841 CAGTGTCTCTGTGAGACCAACTGGGCGCGAGCTCTGTGACAAAGATCTCAATTAATCTGT 900  
Db 1249 CAGTGTCTCTGTGAGACCAACTGGGCGCGAGCTCTGTGACAAAGATCTCAATTAATCTGT 1308  
Qy 901 GGGACTCATCAGCCGCTGTCTCAACGGGGGAACTTTAGCAACACAGGCGCTGACAAATAT 960  
Db 1309 GGGACTCATCAGCCGCTGTCTCAACGGGGGAACTTTAGCAACACAGGCGCTGACAAATAT 1368  
Qy 961 CAGTGTCTCTGCGCTCAGGGGTATTGAGGACCAACTGTGAAATTTGCTGAGACGCGCTGC 1020  
Db 1369 CAGTGTCTCTGCGCTCAGGGGTATTGAGGACCAACTGTGAAATTTGCTGAGACGCGCTGC 1428  
Qy 1021 CTCTGTGATCCCTGTCAACACAGAGCGAGCTGTAAAGGAGACCTCCCTGGGCTTTGAGTGT 1080  
Db 1429 CTCTGTGATCCCTGTCAACACAGAGCGAGCTGTAAAGGAGACCTCCCTGGGCTTTGAGTGT 1488  
Qy 1081 GAGTGTTCCTCCAGGCTGGACCGGCGCCCAATGCTCTCAAAATTTGATGATGCTGTTCTCT 1140  
Db 1489 GAGTGTTCCTCCAGGCTGGACCGGCGCCCAATGCTCTCAAAATTTGATGATGCTGTTCTCT 1548  
Qy 1141 AATAACTGTTCCACAGGCGGCGACCTGCGAGGACCTGGTTAAACGGATTTAAGTGTGTGTC 1200  
Db 1549 AATAACTGTTCCACAGGCGGCGACCTGCGAGGACCTGGTTAAACGGATTTAAGTGTGTGTC 1608  
Qy 1201 CCCCCACAGTGGACTGGGAAACGTCGCAAGTTAGATGCAAAATGAATGTGAGGCGCAACCT 1260  
Db 1609 CCCCCACAGTGGACTGGGAAACGTCGCAAGTTAGATGCAAAATGAATGTGAGGCGCAACCT 1668  
Qy 1261 TGTGTAAACGCGCAAACTCTGTAAAGATCTCATTTGCCAGCTACTACTGCGACTGTCTTTCCC 1320  
Db 1669 TGTGTAAACGCGCAAACTCTGTAAAGATCTCATTTGCCAGCTACTACTGCGACTGTCTTTCCC 1728  
Qy 1321 GGTGATGAGTGGTCAAGATTTGTGACATAAATTAATTAATGACTGCGCTGGCCAGTGTCAAGAT 1380  
Db 1729 GGTGATGAGTGGTCAAGATTTGTGACATAAATTAATTAATGACTGCGCTGGCCAGTGTCAAGAT 1788  
Qy 1381 GAGCCTCTCTGTGCGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACTGGCTATGCA 1440  
Db 1789 GAGCCTCTCTGTGCGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACTGGCTATGCA 1848  
Qy 1441 GGGATFCACTGTGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT 1500  
Db 1849 GGGATFCACTGTGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT 1908  
Qy 1501 CACTGTCAAGTGAATCAACAGATTCAGTGTCTGTGTGCCACTGGTTCTCTGGAAAC 1560  
Db 1909 CACTGTCAAGTGAATCAACAGATTCAGTGTCTGTGTGCCACTGGTTCTCTGGAAAC 1968  
Qy 1561 CTCTGTGAGTGGACATCGATTAATTTGTGAGCCTTAATCCCTGCCAGAACCGTGGCCAGTGC 1620  
Db 1969 CTCTGTGAGTGGACATCGATTAATTTGTGAGCCTTAATCCCTGCCAGAACCGTGGCCAGTGC 2028  
Qy 1621 TACAACCGTGGCAGTGAATTTTCTGCAAGTGTGCCCGGAGGACTATGAGGGCAAGAACTGC 1680

|||||  
2029 TACACCGTCCAGTGACTATTTCTGCAAGTGCCTCCGAGGACTATGAGGGCAGAACTGC 2088  
QY  
1681 TCACACCTGAAAGACCACTGCCGACGACCCCTGTGGAAGTATGACAGCTGCACAGTG 1740  
Db  
2089 TCACACCTGAAAGACCACTGCCGACGACCCCTGTGGAAGTATGACAGCTGCACAGTG 2148  
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1741 GCCATGGCTTCCACGACGACACCTGAAGGGGTGGGTATATTTCTCCCAACGCTGTGGT 1800  
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2149 GCCATGGCTTCCACGACGACACCTGAAGGGGTGGGTATATTTCTCCCAACGCTGTGGT 2208  
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1801 CCTCACGGGAAGTGCAGAGTCACTCGGAGGAGCAAAATTCACCTGTGACTGTATTAACAAAGGC 1860  
Db  
2209 CCTCACGGGAAGTGCAGAGTCACTCGGAGGAGCAAAATTCACCTGTGACTGTATTAACAAAGGC 2268  
QY  
1861 TTCAACGGGAACATACCTGCCATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAGAAAC 1920  
Db  
2269 TTCAACGGGAACATACCTGCCATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAGAAAC 2328  
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2329 GGTGGGACCTTGATCGATGCTGATCACTCCTACAGTGCATCTGTAGTACGGCTGGGAG 2388  
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2041 ACCTGTCCGACCTGTGTCAATGACTCTTACTGTGACTGTAAATAATGGGTGGAAGGAAAG 2100  
Db  
2449 ACCTGTCCGACCTGTGTCAATGACTCTTACTGTGACTGTAAATAATGGGTGGAAGGAAAG 2508  
QY  
2101 ACCTGCCACTCAGTGCAGTGCAGTGCAGGCGCAGCTGCACAAACGGTGGCAGCTGC 2160  
Db  
2509 ACCTGCCACTCAGTGCAGTGCAGTGCAGGCGCAGCTGCACAAACGGTGGCAGCTGC 2568  
QY  
2161 TATGATCAGGGGATGCTTTTAAGTGCATGTGCTCGCGCTGGGAAGGAAACAACTGT 2220  
Db  
2569 TATGATCAGGGGATGCTTTTAAGTGCATGTGCTCGCGCTGGGAAGGAAACAACTGT 2628  
QY  
2221 AACATAGCCGAAACAGTGTGCTGCTGCCAACCCCTGCCAATATGGGGGACATGTGTG 2280  
Db  
2629 AACATAGCCGAAACAGTGTGCTGCTGCCAACCCCTGCCAATATGGGGGACATGTGTG 2688  
QY  
2281 GTCAACGGCGAGTCTTTTACGTGCTGTGCAGGAGAGGCTGGGAGGGCCCATCTGTGCT 2340  
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2809 GACAACTGGTACCGGTGCAATGTGCCCGGGTTTTGTGGGCGCGACTGCAGAAATAAAC 2868  
QY  
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Db  
2869 ATCAATGAATCCAGTCTTACCTTGTGCTTTGGAGGACCTGTGTGGATGAGATCAAT 2928  
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2521 GGCTACCGGTGTGTGCTGCTCCAGGGGACAGTGTGCTCAAGTGCAGAGAGTTTCAGGG 2580  
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Db  
3049 AATACCTGCCAGTGCCTGAATGGAGCGATCGCTGCTCAAGGTTCTGTGTGGCCCTCGA 3108  
QY  
2701 CCTTGCCTGTCTCCAAAGAGGGCAGAGCTGAGTGGCCAGCGGCGAGCTGCATCCCCATC 2760  
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Db  
3109 CCTTGCTGCTCCACAAAGGGCAGACGAGTGCCCCAGCGGCGAGAGCTGCATCCCCATC 3168  
QY  
2761 CTGGACGACGAGTGTCTGTCACCCCTGCACCTGCTGCTGGGCGAGTGTCCGTTCTCCAGT 2820  
Db  
3169 CTGGACGACGAGTGTCTGTCACCCCTGCACCTGCTGCTGGGCGAGTGTCCGTTCTCCAGT 3228  
QY  
2821 CTCCAGCCGCTGAAGACAAAGTGACCTCTGACTCTCTATTACCAGGATAACTGTGCGAAC 2880  
Db  
3229 CTCCAGCCGCTGAAGACAAAGTGACCTCTGACTCTCTATTACCAGGATAACTGTGCGAAC 3288  
QY  
2881 ATCACATTTACCTTTAAACAAAGGAGATGTCACAGGCTCTTACTACGGAGCACATTTCG 2940  
Db  
3289 ATCACATTTACCTTTAAACAAAGGAGATGTCACAGGCTCTTACTACGGAGCACATTTCG 3348  
QY  
2941 AGTGAATTCAGGAAATTTGAATATTTTGAAGAATGTTTCCGCTGAAATATCAATCTACATC 3000  
Db  
3349 AGTGAATTCAGGAAATTTGAATATTTTGAAGAATGTTTCCGCTGAAATATCAATCTACATC 3408  
QY  
3001 GCTTGGAGCTTCCCTTTACGCGAAACAATGAAATAACATGTGGCCATTTCTGCTGAAGAT 3060  
Db  
3409 GCTTGGAGCTTCCCTTTACGCGAAACAATGAAATAACATGTGGCCATTTCTGCTGAAGAT 3468  
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3061 ATACGGGATGATGGGAAACCCGATCAAGGAAATCACTGAACAAATAATGATCTTGTAGT 3120  
Db  
3469 ATACGGGATGATGGGAAACCCGATCAAGGAAATCACTGAACAAATAATGATCTTGTAGT 3528  
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Db  
3529 AAACGTGATGGAACACAGCTCGCTGATTGCTGCGTTGCAAGTAAGAGTTCAGAGCGG 3588  
QY  
3181 CCTCTCAAGAAACAGAAACAGATTTCTTGTTCCTTCTGCTGAGCTCTGCTTTAACTGTGGCT 3240  
Db  
3589 CCTCTCAAGAAACAGAAACAGATTTCTTGTTCCTTCTGCTGAGCTCTGCTTTAACTGTGGCT 3648  
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3241 TGGATCTGTGTGTGTGACGCGCTTCTACTGTGTGCTGCGGAAGCGCGGAAAGCGGCG 3300  
Db  
3649 TGGATCTGTGTGTGTGACGCGCTTCTACTGTGTGCTGCGGAAGCGCGGAAAGCGGCG 3708  
QY  
3301 AGCCACACACACTCAGCTCTGAGGACAAACACCAACAAACCTGCGGGAGCAGCTGAAC 3360  
Db  
3709 AGCCACACACACTCAGCTCTGAGGACAAACACCAACAAACCTGCGGGAGCAGCTGAAC 3768  
QY  
3361 CAGATCAAAAAACCCCATTTGAGAAACATTTGGGCGCAACACAGCTCCCCATCAAGGATTACGAG 3420  
Db  
3769 CAGATCAAAAAACCCCATTTGAGAAACATTTGGGCGCAACACAGCTCCCCATCAAGGATTACGAG 3828  
QY  
3421 AACAGAACTCCAAAATGTCTAAAATAAGGACACAAATTTCTGAAAGTAGAAGAGGACGAC 3480  
Db  
3829 AACAGAACTCCAAAATGTCTAAAATAAGGACACAAATTTCTGAAAGTAGAAGAGGACGAC 3888  
QY  
3481 ATGGACAAACACCAAGCAGAAAGCCCGTTTGGCAAGCAGCGCGGTATACGCTGGTAGAC 3540  
Db  
3889 ATGGACAAACACCAAGCAGAAAGCCCGTTTGGCAAGCAGCGCGGTATACGCTGGTAGAC 3948  
QY  
3541 AGAGAAGAGAGCGCCCAACCGCACGCGCCAGCAAAAACACCCAACTGGACAAAACAAACAG 3600  
Db  
3949 AGAGAAGAGAGCGCCCAACCGCACGCGCCAGCAAAAACACCCAACTGGACAAAACAAACAG 4008  
QY  
3601 GACAAACAGAGACTTGGAAAGTGCCAGAGCTTTAAACCCGAATGGAGTACATCGTATAG 3657  
Db  
4009 GACAAACAGAGACTTGGAAAGTGCCAGAGCTTTAAACCCGAATGGAGTACATCGTATAG 4065

RESULT 10  
US-08-400-159-5  
; Sequence 5, Application US/08400159  
; Patent No. 5869282  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos M.P.  
; APPLICANT: Lewis, Julian H.  
; APPLICANT: Myat, Anna M.  
; APPLICANT: Fleming, Robert J.



QY	1501	CACTGTGAGAAATCAACAGATCCAGTGTCTGTGTCCTCACTGGTTTCTCTGGAAC	1560
DB	1871	CATGTGAGAAATCAACAGATCCAGTGTCTGTGTCCTCACTGGTTTCTCTGGAAC	1930
QY	1561	CTCTGTGAGTGAATCGAATTAATGAGCCTAATCCCTGCGAGAACGGTGGCCAGTGC	1620
DB	1931	CTCTGTGAGTGAATCGAATTAATGAGCCTAATCCCTGCGAGAACGGTGGCCAGTGC	1990
QY	1621	TACAAACGGTCCAGTGAATTTCTGCAAGTGCCTGAGGACTATGAGGCAAGACTGC	1680
DB	1991	TACAAACGGTCCAGTGAATTTCTGCAAGTGCCTGAGGACTATGAGGCAAGACTGC	2050
QY	1681	TCACACCTGAAAGACCACTGCGCAGACACCCCTGTGAACTGATGACAGCTGCACAGTG	1740
DB	2051	TCACACCTGAAAGACCACTGCGCAGACACCCCTGTGAACTGATGACAGCTGCACAGTG	2110
QY	1741	GCCATGGCTTCCAAACGACACACCTGAAAGGGGTGGGTATATTTCTCCAAACGTCTGTGGT	1800
DB	2111	GCCATGGCTTCCAAACGACACACCTGAAAGGGGTGGGTATATTTCTCCAAACGTCTGTGGT	2170
QY	1801	CCTCAGGGAGTGCAGAGTCACTGCGGAGGCAATTTCACTGTGACTGTGAATCAAGGC	1860
DB	2171	CCTCAGGGAGTGCAGAGTCACTGCGGAGGCAATTTCACTGTGACTGTGAATCAAGGC	2230
QY	1861	TTCAACGGGAACATACTGCCATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAAAC	1920
DB	2231	TTCAACGGGAACATACTGCCATGAAATATTAATGACTGTGAGAGCAACCCCTGTGAAAC	2290
QY	1921	GGTGGCACTTGCAATCGATGTGCACTCTCAAGTGCATCTGTAGTGAACGGTGGAG	1980
DB	2291	GGTGGCACTTGCAATCGATGTGCACTCTCAAGTGCATCTGTAGTGAACGGTGGAG	2350
QY	1981	GGGGCTTACTGTGAAACCAATATTAATGACTGTGAGAGCAACCCCTGCGCAATGGGGC	2040
DB	2351	GGGGCTTACTGTGAAACCAATATTAATGACTGTGAGAGCAACCCCTGCGCAATGGGGC	2410
QY	2041	ACGTGTGCGGACCTGTGCAATGACTCTTAATGACTGTGAAATGGGTGAAAGGAAAG	2100
DB	2411	ACGTGTGCGGACCTGTGCAATGACTCTTAATGACTGTGAAATGGGTGAAAGGAAAG	2470
QY	2101	ACCTGCCACTCAGGTGACAGTGTGATGAGGCCACGTGCAACAAACGGTGGCACTGC	2160
DB	2471	ACCTGCCACTCAGGTGACAGTGTGATGAGGCCACGTGCAACAAACGGTGGCACTGC	2530
QY	2161	TATGATGAGGGGATGCTTTTAAGTGCATGTGTCTGCGGCTGGGAGGAAACAACTGT	2220
DB	2531	TATGATGAGGGGATGCTTTTAAGTGCATGTGTCTGCGGCTGGGAGGAAACAACTGT	2590
QY	2221	AACATAGCCGAAACAGTGTGCTGCCCAACCCCTGCCATATGAGGGGCAATGTGTG	2280
DB	2591	AACATAGCCGAAACAGTGTGCTGCCCAACCCCTGCCATATGAGGGGCAATGTGTG	2650
QY	2281	GTCAACGGGAGTCTTTAAGTGCATGTGTCTGCAAGGAGGCTGGAGGGGCCATCTGTGCT	2340
DB	2651	GTCAACGGGAGTCTTTAAGTGCATGTGTCTGCAAGGAGGCTGGAGGGGCCATCTGTGCT	2710
QY	2341	CAGATACCAATGACTGCGCCCTCATCCCTGTGTTACAAACGGGCACTGTGTGATGGA	2400
DB	2711	CAGATACCAATGACTGCGCCCTCATCCCTGTGTTACAAACGGGCACTGTGTGATGGA	2770
QY	2401	GACAACTGGTACCGGTGCAATGTGCGCCGGGTTTGTGCGGGCCGACTGCGAGAAATAAC	2460
DB	2771	GACAACTGGTACCGGTGCAATGTGCGCCGGGTTTGTGCGGGCCGACTGCGAGAAATAAC	2830
QY	2461	ATCAATGAATGCCAGTCTTCACTTGTGCTTGTGAGCGACCTGTGTGATGAGATCAAT	2520
DB	2831	ATCAATGAATGCCAGTCTTCACTTGTGCTTGTGAGCGACCTGTGTGATGAGATCAAT	2890
QY	2521	GGCTACCGGTGTGCTGCGCTCCAGGGGCAAGTGTGCGGAGTTCAGGG	2580
DB	2891	GGCTACCGGTGTGCTGCGCTCCAGGGGCAAGTGTGCGGAGTTCAGGG	2950
QY	2581	AGACCTTGCAATCACCATGGGAGTGTGATACAGATGGGGCAAAATGGGATGATGACTGT	2640

RESULT 11

DB	2951	AGACCTTGCAATCACCATGGGAGTGTGATACAGATGGGGCAAAATGGGATGATGACTGT	3010
QY	2641	AATACCTGCAGTGCCTGAAATGGAACGGATCGCTCTCAAGGTCTGGTGTGGCCCTCGA	2700
DB	3011	AATACCTGCAGTGCCTGAAATGGAACGGATCGCTCTCAAGGTCTGGTGTGGCCCTCGA	3070
QY	2701	CCTTGCTCTCTCCAAAGGGCAGCAGAGTGCCTCAGGGGAGAGCTGCATCCCCATC	2760
DB	3071	CCTTGCTCTCTCCAAAGGGCAGCAGAGTGCCTCAGGGGAGAGCTGCATCCCCATC	3130
QY	2761	CTGGACGACCAAGTCTGCTTCCACCTCGACTGTGGTGTGGGAGTGTGGTCTTCCAGT	2820
DB	3131	CTGGACGACCAAGTCTGCTTCCACCTCGACTGTGGTGTGGGAGTGTGGTCTTCCAGT	3190
QY	2821	CTCCAGCCGTGAGGAAAGTGCACCTCTGACTCTTATTTACCAGATTAACCTGTGGAAAC	2880
DB	3191	CTCCAGCCGTGAGGAAAGTGCACCTCTGACTCTTATTTACCAGATTAACCTGTGGAAAC	3250
QY	2881	ATCACATTTTACCTTTAAACAGGAGATGATGTCAACAGGTCTTACTACGGAGCACTTTGC	2940
DB	3251	ATCACATTTTACCTTTAAACAGGAGATGATGTCAACAGGTCTTACTACGGAGCACTTTGC	3310
QY	2941	AGTGAATGAGGAAATTTGAATATTTTGAAGAAATGTTTCCGCTGAATATTTCAATCTCATC	3000
DB	3311	AGTGAATGAGGAAATTTGAATATTTTGAAGAAATGTTTCCGCTGAATATTTCAATCTCATC	3370
QY	3001	GCTTGCGAGCTTCCCTTTCAGCGAACAAATGAATACATGTGGCCATTTCTGCTGAAGAT	3060
DB	3371	GCTTGCGAGCTTCCCTTTCAGCGAACAAATGAATACATGTGGCCATTTCTGCTGAAGAT	3430
QY	3061	ATACCGGATGATGGGAAACCCGATCAAGGAAATCACTGACAAAATAATTCGATCTTTTGTAGT	3120
DB	3431	ATACCGGATGATGGGAAACCCGATCAAGGAAATCACTGACAAAATAATTCGATCTTTTGTAGT	3490
QY	3121	AAAACGTGTGAGAAACAGTCTGCTGTGCTGCTGCGTTCGAGAAATGATGAGTTCAGAGCGG	3180
DB	3491	AAAACGTGTGAGAAACAGTCTGCTGTGCTGCGTTCGAGAAATGATGAGTTCAGAGCGG	3550
QY	3181	CCTCTGAGAACAGACAGATTTCTTGTGCTTCCCTGCTGAGCTCTGTCTTAACTGTGGCT	3240
DB	3551	CCTCTGAGAACAGACAGATTTCTTGTGCTTCCCTGCTGAGCTCTGTCTTAACTGTGGCT	3610
QY	3241	TGATCTGTGTGCTGAGCGCTTCTACTGTGCTGCTGCGGAGGCGGAGGAGCGGCGC	3300
DB	3611	TGATCTGTGTGCTGAGCGCTTCTACTGTGCTGCTGCGGAGGCGGAGGAGCGGCGC	3670
QY	3301	AGCCACACACACTCAGCCTCTGAGGACAAACCAACAAACCGTGGGAGGAGCTGAAC	3360
DB	3671	AGCCACACACACTCAGCCTCTGAGGACAAACCAACAAACCGTGGGAGGAGCTGAAC	3730
QY	3361	CAGATCAAAAACCCCATTTGAGAACCATGGGGCCAAACCGTCCCCCATCAAGGATTACGAG	3420
DB	3731	CAGATCAAAAACCCCATTTGAGAACCATGGGGCCAAACCGTCCCCCATCAAGGATTACGAG	3790
QY	3421	AACAAGAACTTCAAAATGTCTAAAAAAGGACACACAATTTCTGAAGTAGAAGGAGGACAC	3480
DB	3791	AACAAGAACTTCAAAATGTCTAAAAAAGGACACACAATTTCTGAAGTAGAAGGAGGACAC	3850
QY	3481	ATGGACAAAACCAACAGAGAAAGCCCGTTTGGAGAGCAGCGCGGCTATACGCTGGTAGAC	3540
DB	3851	ATGGACAAAACCAACAGAGAAAGCCCGTTTGGAGAGCAGCGCGGCTATACGCTGGTAGAC	3910
QY	3541	AGAGAGAGAGAGCCCGCCCAACGGCAGCAACCAACCAACCTGACAAAACAAACAG	3600
DB	3911	AGAGAGAGAGAGCCCGCCCAACGGCAGCAACCAACCAACCTGACAAAACAAACAG	3970
QY	3601	GACAAACAGAGACTTGGAAAGTGGCCAGAGCTTAAACCCGAATGGAGTACATCGTATAG	3657
DB	3971	GACAAACAGAGACTTGGAAAGTGGCCAGAGCTTAAACCCGAATGGAGTACATCGTATAG	4027

Query Match	99.7%	Score 3646.2;	DB 3;	Length 6464;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 3648; Conservative	3;	Mismatches 6;	Indels 0;	Gaps 0;

  

Qy	1	ATGGGTTCCCAACGGACRGGGGCGGTTCGGGGCCCCCTAAGCCTCTGCTGCCCTG	60
		:	
Db	371	ATGGGTTCCCAACGGACACGGGGCGGTTCGGGGCCCCCTAAGCCTCTGCTGCCCTG	430
		:	
Qy	61	CTCTGTGCCTTCCGAGGCCAAAGTGTTGGGGCCTCGGTCAGTTCGAGTTGGAGATCCTG	120
		:	
Db	431	CTCTGTGCCTTCCGAGCCNAGTGTGTGGGGCCTCGGTCAGTTCGAGTTGGAGATCCTG	490
		:	
Qy	121	TCCATGCAGAACGTGAACGGGGAGCTGCAGAACCGGAACTGCTGCGGGCGGCCCGGAAC	180
		:	
Db	491	TCCA TG CAG AAC GT GA A CG GG G AG CT GC AG AAC GG G AA CT CT GC GG CG GG CC CG G AAC	550
		:	
Qy	181	CCGGGAGACCGCAAGTGCACC CGG AC GAG GTGACA CAT ACT TC AA AG TGT GCT CAAG	240
		:	
Db	551	CCGGGAGACCGCAAGTGCACC CGG AC GAG GTGACA CAT ACT TC AA AG TGT GCT CAAG	610
		:	
Qy	241	GAGTATCAGTCCCGCTCACGGCCGGGGGCCCTGCAGCTTCGGCTCAGGGTCCACGCCT	300



QY	1381	GAGCCTCCTGTCGGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGCTATGCA	1440
Db	1751	GAGCCTCCTGTCGGGATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGCTATGCA	1810
QY	1441	GGCGATCACTGTGAGAGACATCGCATGAATGTGCCAGCAACCCCTGTGTTGAATGGGGGT	1500
Db	1811	GGCGATCACTGTGAGAGACATCGCATGAATGTGCCAGCAACCCCTGTGTTGAATGGGGGT	1870
QY	1501	CACGTGCAGAAATGAAATCAAACAGATTCCAGTGTCTGTGTCCCACTGTGTTTCTCTGGAAC	1560
Db	1871	CACGTGCAGAAATGAAATCAAACAGATTCCAGTGTCTGTGTCCCACTGTGTTTCTCTGGAAC	1930
QY	1561	CTCTGTGAGTGCATCGATTAATTTGTAGCGCTAAATCCCTGCCAGAACGGTGGCCAGTGC	1620
Db	1931	CTCTGTGAGTGCATCGATTAATTTGTAGCGCTAAATCCCTGCCAGAACGGTGGCCAGTGC	1990
QY	1621	TACAACCGTCCAGTGTACTATTTCTGCAAGTGGCCCGAGGACTATGAGGGCAAGAACTGC	1680
Db	1991	TACAACCGTCCAGTGTACTATTTCTGCAAGTGGCCCGAGGACTATGAGGGCAAGAACTGC	2050
QY	1681	TCACACCTGAAAGACCACTGCCGACAGACCCCTGTGTGAAGTGAATGACAGCTGCACAGTG	1740
Db	2051	TCACACCTGAAAGACCACTGCCGACAGACCCCTGTGTGAAGTGAATGACAGCTGCACAGTG	2110
QY	1741	GCCATGGCTTCCACGACACACCTGGAAGGGGTGGGTATATTTCCCTCCACCGTCTGTGGT	1800
Db	2111	GCCATGGCTTCCACGACACACCTGGAAGGGGTGGGTATATTTCCCTCCACCGTCTGTGGT	2170
QY	1801	CCTCAGCGGAAGTGCAGAGTCACTCGGGAGGCAAAATTCACCTGTGTGACTGTAAACAAAGGC	1860
Db	2171	CCTCAGCGGAAGTGCAGAGTCACTCGGGAGGCAAAATTCACCTGTGTGACTGTAAACAAAGGC	2230
QY	1861	TTCAACGGGAACATACTGCCATGAAATTAATGACTGTGTGAGAGCAACCCCTGTGTAGAAC	1920
Db	2231	TTCAACGGGAACATACTGCCATGAAATTAATGACTGTGTGAGAGCAACCCCTGTGTAGAAC	2290
QY	1921	GGTGGCACTTCGATCGATGTGTCAACTCTACAGTGTGATCTGTAGTGCAGCTGGGAG	1980
Db	2291	GGTGGCACTTCGATCGATGTGTCAACTCTACAGTGTGATCTGTAGTGCAGCTGGGAG	2350
QY	1981	GGGSCCTACTGTGAAACCAATATTAATGACTGTGAGAGCAACCCCTGCCCAATGGGGGC	2040
Db	2351	GGGSCCTACTGTGAAACCAATATTAATGACTGTGAGAGCAACCCCTGCCCAATGGGGGC	2410
QY	2041	ACGTGTCCGACCTGTGTCAATGACTTCTAATGACTGTGTAAATATGGGTGAAAGGAAG	2100
Db	2411	ACGTGTCCGACCTGTGTCAATGACTTCTAATGACTGTGTAAATATGGGTGAAAGGAAG	2470
QY	2101	ACCTGCCACTCAGTGCAGTGTGATGAGGCGACGTGCAACACGGTGGCACCTGC	2160
Db	2471	ACCTGCCACTCAGTGCAGTGTGATGAGGCGACGTGCAACACGGTGGCACCTGC	2530
QY	2161	TATGATGAGGGGATGCTTTTAAGTGCATGTCTCGCGCTGGGAAGGAACAACTGT	2220
Db	2531	TATGATGAGGGGATGCTTTTAAGTGCATGTCTCGCGCTGGGAAGGAACAACTGT	2590
QY	2221	AACATAGCCCGAAACAGTAGTGCCTGCCAACCCCTGCCAATATGGGGGCACATGTGTG	2280
Db	2591	AACATAGCCCGAAACAGTAGTGCCTGCCAACCCCTGCCAATATGGGGGCACATGTGTG	2650
QY	2281	GTCAACGGCGAGTCTTTTACGTGCGTCTGCAGGAAGGCTGGGAGGGGCCCATCTGTGCT	2340
Db	2651	GTCAACGGCGAGTCTTTTACGTGCGTCTGCAGGAAGGCTGGGAGGGGCCCATCTGTGCT	2710
QY	2341	CAGAAATACCAATGACTGCAGCCCTCATCCCTGTTTACAACACGGCGACCTGTGTGATGGA	2400
Db	2711	CAGAAATACCAATGACTGCAGCCCTCATCCCTGTTTACAACACGGCGACCTGTGTGATGGA	2770
QY	2401	GACAACTGGTACCGGTGCGAATGTGCCCGGGTTTTGCTGGGCCCGACTGCGAGAAATAAC	2460
Db	2771	GACAACTGGTACCGGTGCGAATGTGCCCGGGTTTTGCTGGGCCCGACTGCGAGAAATAAC	2830

QY	2461	ATCAATGAATGCCAGTCTTTCACCTTGTGCTTTGGAGCGACCTGTGTGATGAGATCAAT	2520
Db	2831	ATCAATGAATGCCAGTCTTTCACCTTGTGCTTTGGAGCGACCTGTGTGATGAGATCAAT	2890
QY	2521	GGCTACCGGTGTGTCTGCGCTCCAGGGCACAGTGTGTGCCAAAGTGTGCAGGAAGTTTCAGGG	2580
Db	2891	GGCTACCGGTGTGTCTGCGCTCCAGGGCACAGTGTGTGCCAAAGTGTGCAGGAAGTTTCAGGG	2950
QY	2581	AGACCTTGTGATCACCANTGGGGAGTGTATACAGATGGGGGCCAAAATGGGGATGATGACTGT	2640
Db	2951	AGACCTTGTGATCACCANTGGGGAGTGTATACAGATGGGGGCCAAAATGGGGATGATGACTGT	3010
QY	2641	AATACCTGCCAGTCCCTGAATGGAGCGGATCGCTGTCTCAAAGGTCTGTGTGTGCGCCCTCGA	2700
Db	3011	AATACCTGCCAGTCCCTGAATGGAGCGGATCGCTGTCTCAAAGGTCTGTGTGTGCGCCCTCGA	3070
QY	2701	CCTTGTCTGCTCCAAAAGGGCACAGGAGTGTGCCCCAGGGGGCAGAGCTGTCATCCCCATC	2760
Db	3071	CCTTGTCTGCTCCAAAAGGGCACAGGAGTGTGCCCCAGGGGGCAGAGCTGTCATCCCCATC	3130
QY	2761	CTGGACGACAGTGTCTGCTCCACCCCTGCACCTGTGTGTGGCGAGTGTGCGTCTTCCAGT	2820
Db	3131	CTGGACGACAGTGTCTGCTCCACCCCTGCACCTGTGTGTGGCGAGTGTGCGTCTTCCAGT	3190
QY	2821	CTCCAGCCGTGAAAGCAAAAGTGCACCTCTGACTCTCTATTTACCAGGATAACTGTGCGAAC	2880
Db	3191	CTCCAGCCGTGAAAGCAAAAGTGCACCTCTGACTCTCTATTTACCAGGATAACTGTGCGAAC	3250
QY	2881	ATCACATTTTACCTTTAAACAGGAGATGTGTCAACAGGTCTTACTACGGAGCACTTTGCT	2940
Db	3251	ATCACATTTTACCTTTAAACAGGAGATGTGTCAACAGGTCTTACTACGGAGCACTTTGCT	3310
QY	2941	AGTGAATTTAGGAAATTTGAATATTTTGAAGAATGTTTCCGCTGAATATTTCAATCTACATC	3000
Db	3311	AGTGAATTTAGGAAATTTGAATATTTTGAAGAATGTTTCCGCTGAATATTTCAATCTACATC	3370
QY	3001	GCTTGCAGGCTTCCCTTTCAGCGAAACAATGAAATACATGTGCGCAATTTCTGCTGAAGAT	3060
Db	3371	GCTTGCAGGCTTCCCTTTCAGCGAAACAATGAAATACATGTGCGCAATTTCTGCTGAAGAT	3430
QY	3061	ATACGGGATGATGGGAACCCGATCAAGGAAATCACTGACAAAATATTCGATCTTGTGTAGT	3120
Db	3431	ATACGGGATGATGGGAACCCGATCAAGGAAATCACTGACAAAATATTCGATCTTGTGTAGT	3490
QY	3121	AAACGTGTGAAACACAGCTCGCTGATTTGTCGCGTTGCGAAGTGAAGAGTTTCAGAGCGG	3180
Db	3491	AAACGTGTGAAACACAGCTCGCTGATTTGTCGCGTTGCGAAGTGAAGAGTTTCAGAGCGG	3550
QY	3181	CCTCTGAAGAACAGAACAGATTTTCTTGTTCCTTGTCTGAGCTCTGTCTTAACTGTGGCT	3240
Db	3551	CCTCTGAAGAACAGAACAGATTTTCTTGTTCCTTGTCTGAGCTCTGTCTTAACTGTGGCT	3610
QY	3241	TGGATCTGTTGCTTGTGTGACGGCTTCTACTGTGTGCTGCGAAGCGGGCGAAGCCGGGC	3300
Db	3611	TGGATCTGTTGCTTGTGTGACGGCTTCTACTGTGTGCTGCGAAGCGGGCGAAGCCGGGC	3670
QY	3301	AGCCACACACTCAGCTCTGAGGACCAACACCAACCAACCTGCGGGAGCAGCTCAAC	3360
Db	3671	AGCCACACACTCAGCTCTGAGGACCAACACCAACCAACCTGCGGGAGCAGCTCAAC	3730
QY	3361	CAGATCAAAAAACCCCATTTGAGAAACATGGGGCCAAACACGCTCCCATCAAGGATTAAGAG	3420
Db	3731	CAGATCAAAAAACCCCATTTGAGAAACATGGGGCCAAACACGCTCCCATCAAGGATTAAGAG	3790
QY	3421	AACAAGAACTCCAAAAATGCTTAAAAATAAGGACACAAATTTCTGAAGTGAGAGGAGAC	3480
Db	3791	AACAAGAACTCCAAAAATGCTTAAAAATAAGGACACAAATTTCTGAAGTGAGAGGAGAC	3850
QY	3481	ATGGACAAAACACGAGCAAGCCCGTTTGGCAAGCAGCGCGGTATACCTGCTGTAGAC	3540
Db	3851	ATGGACAAAACACGAGCAAGCCCGTTTGGCAAGCAGCGCGGTATACCTGCTGTAGAC	3910
QY	3541	AGAGAAAGAAAGCCCCCAACCGGCAACCGCCGACAAAAACACCCAACTGGACAAAACAAACAG	3600





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Db	1571	CCCCCAGTGGAGCTGGGAAAACGTGCGAGTTAGATGCAAAATGAATGTGAGGCCAAACCT	1630
Qy	1261	TGTGTAAACGCCAAATCCTGTGAAGAAATCTCATTTGCCAGCTACTACTGCGACTGTCTTTCCC	1320
Db	1631	TGTGTAAACGCCAAATCCTGTGAAGAAATCTCATTTGCCAGCTACTACTGCGACTGTCTTTCCC	1690
Qy	1321	GGCTGGATGGGTGAGAAATGTGACATAAAATATTAATGACTGCTTGGCCAGTGTGAGAAAT	1380
Db	1691	GGCTGGATGGGTGAGAAATGTGACATAAAATATTAATGACTGCTTGGCCAGTGTGAGAAAT	1750
Qy	1381	GACGCTCTCTGTGGGAAATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGGCTATGCA	1440
Db	1751	GACGCTCTCTGTGGGAAATTTGGTTAATGGTTATCGCTGTATCTGTCCACCTGGCTATGCA	1810
Qy	1441	GGCGATCACTGTGAGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT	1500
Db	1811	GGCGATCACTGTGAGAGAGACATCGATGAATGTGCCAGCAACCCCTGTTTGAATGGGGGT	1870
Qy	1501	CACGTGCAGAAATCAACAGAAATCCAGTGTCTGTGTGCCACTGTGTTCTCTGGAAC	1560
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Qy	1561	CTCTGTGAGTGGACATCGATTTATTTGTGAGCCTAATCCCTGCCAGAACGGTGGCCAGTGC	1620
Db	1931	CTCTGTGAGTGGACATCGATTTATTTGTGAGCCTAATCCCTGCCAGAACGGTGGCCAGTGC	1990
Qy	1621	TACAAACGGTGCAGTGAATTTCTGCAAGTGGCCCGAGGACTATGAGGGCAAGAACTGC	1680
Db	1991	TACAAACGGTGCAGTGAATTTCTGCAAGTGGCCCGAGGACTATGAGGGCAAGAACTGC	2050
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Db	2051	TCACACCTGAAAGACCACTGCGCGACGACCCCTGTGAAAGTGAATGACGTGCACAGTG	2110
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Db	2171	CCTCACGGGAAGTGCAGAGTCACTCGGGAGGCAAAATTCACCTGTGACTGTGTAAACAAAGGC	2230
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Db	2411	ACGTGTCCGCACTGTGCAATGACTTTCTGAGCTGTGTAATAAATGGGTGAAAGGAAAG	2470
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Db	2531	TATGATGAGGGGATGCTTTTAAAGTGCATGTGTCTCTGGCGCTGGGAGGAAACACCTGT	2590
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Db	2591	AACATAGCCCCGAAACAGTGTGCTGCCCAACCCCTGCCCAATATGGGGGCAATGTGTG	2650

Qy	2281	GTCAACGGCGAGTCTTTTACGTGCGTCTGCAAGAAAGGTGGAGGGGCCATCTGTGCT	2340
Db	2651	GTCAACGGCGAGTCTTTTACGTGCGTCTGCAAGAAAGGTGGAGGGGCCATCTGTGCT	2710
Qy	2341	CAGAAATCAATGACTGCGAGCCCTCATCCCTGTGTTACAAACGCGGCACTGTGTGGATGGA	2400
Db	2711	CAGAAATCAATGACTGCGAGCCCTCATCCCTGTGTTACAAACGCGGCACTGTGTGGATGGA	2770
Qy	2401	GACAACTGGTACCGGTGCGAAATGTGCCCGGGTTTTGCTGGGCCCGACATGCAGAAATAAAC	2460
Db	2771	GACAACTGGTACCGGTGCGAAATGTGCCCGGGTTTTGCTGGGCCCGACATGCAGAAATAAAC	2830
Qy	2461	ATCAATGAATGCCAGTCTTTCACCTTGTGCTTTTGGAGCGACCTGTGTGGATGAGATCAAT	2520
Db	2831	ATCAATGAATGCCAGTCTTTCACCTTGTGCTTTTGGAGCGACCTGTGTGGATGAGATCAAT	2890
Qy	2521	GGCTACCGGTGTGTCTGCCCTCCAGGGCAAGTGGTGCMAAGTGCACGGAAGTTTCAGGG	2580
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Db	3011	AATACCTTGCAGTCCCTGAAATGAGCGGATCGCCTGTCTCAAAGGTCTGGTGTGGCCCTCGA	3070
Qy	2701	CCTTGTCTGTCTCAAAAGGGCAAGGAGTGGCCCGAGGGGCGAGAGCTGCATCCCCATC	2760
Db	3071	CCTTGTCTGTCTCAAAAGGGCAAGGAGTGGCCCGAGGGGCGAGAGCTGCATCCCCATC	3130
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Db	3311	AGTGAATTTGAGGAATTTGAATATTTTGAAGAAATTTTCCGCTGAAATTTCAATCTCATC	3370
Qy	3001	GCTTGCAGGCTTCCCTTCCAGCGAAACAAATGAAATACATGTGGCCATTTCTGTGAAAGAT	3060
Db	3371	GCTTGCAGGCTTCCCTTCCAGCGAAACAAATGAAATACATGTGGCCATTTCTGTGAAAGAT	3430
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Qy	3121	AAAGCTGATGGAACACCTCGCTGATTCGCGCTTCCAGAGTTAAGAGTTTCAGAGCGG	3180
Db	3491	AAAGCTGATGGAACACCTCGCTGATTCGCGCTTCCAGAGTTAAGAGTTTCAGAGCGG	3550
Qy	3181	CCTCTGAAGAACCAAGACAGATTTTCTTGTTCCTTGTGTGAGCTCTGTCTTAACTGTGGCT	3240
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Qy	3241	TGGATCTGTTGCTTGTGTGACGGCCCTTCTACTGTGTGCTTGGGAGCGCGGAAACCCGGGC	3300
Db	3611	TGGATCTGTTGCTTGTGTGACGGCCCTTCTACTGTGTGCTTGGGAGCGCGGAAACCCGGGC	3670
Qy	3301	AGCCACACACACTCAGCTCTGTGAGGACAAACACCAACCAACCTGCGGGAGCAGCTGAAC	3360
Db	3671	AGCCACACACACTCAGCTCTGTGAGGACAAACACCAACCAACCTGCGGGAGCAGCTGAAC	3730
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RESULT 13
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; Sequence 3, Application US/09310685
; Patent No. 6887475
; GENERAL INFORMATION:
; APPLICANT: Lamb, Jonathan R
; APPLICANT: Dallman, Margaret J
; APPLICANT: Hoyne, Gerard F
; TITLE OF INVENTION: No. 6887475ch
; FILE REFERENCE: 674525-2001
; CURRENT APPLICATION NUMBER: US/09/310,685
; CURRENT FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: GB 9623236.8
; PRIOR FILING DATE: 1996-11-07
; PRIOR APPLICATION NUMBER: GB 9715674.9
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: GB 9719350.2
; PRIOR FILING DATE: 1997-09-11
; PRIOR APPLICATION NUMBER: PCT/GB97/03058
; PRIOR FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 6464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-310-685-3

Query Match 99.7%; Score 3646.2; DB 3; Length 6464;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3648; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Qy 3121 AAAAGTGAAGAAACAGCTCGCTGATTTGCTGCGTTGAGAAAGTAAAGATTCAGAGCGG 3180  
Db 3491 AAAAGTGAAGAAACAGCTCGCTGATTTGCTGCGTTGAGAAAGTAAAGATTCAGAGCGG 3550  
Qy 3181 CCTCTGAAGAACAGAACAGATTTCTGTTTCCCTTGTCTGAGCTCTGTCTTAACTGTGCT 3240  
Db 3551 CCTCTGAAGAACAGAACAGATTTCTGTTTCCCTTGTCTGAGCTCTGTCTTAACTGTGCT 3610  
Qy 3241 TGGATCTGTTGCTTGTGACGGCTTCTACTGTGTGCTGCGGAAGCGCGGAAGCCGGGC 3300  
Db 3611 TGGATCTGTTGCTTGTGACGGCTTCTACTGTGTGCTGCGGAAGCGCGGAAGCCGGGC 3670  
Qy 3301 AGCCACACACACTCAGCTCTGAGGACAAACCAACCAACCAACCGTGCAGGAGCTGAAC 3360  
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Qy 3421 AACAAAGAACTCCAAAAATGCTTAAATAAGGACACACAATTTCTGAAGTAGAAGAGAGAGAC 3480  
Db 3791 AACAAAGAACTCCAAAAATGCTTAAATAAGGACACACAATTTCTGAAGTAGAAGAGAGAGAC 3850  
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Db 3851 ATGGACAAAAACCAAGCAGAAAGCCCGTTTGGCAAGCAGCGCGGCTATACGCTGGTAGAC 3910  
Qy 3541 AGAGAAAG 3600  
Db 3911 AGAGAAAG 3970

QY 3501 GACACAGAGACTTGGAAAGTGCCAGAGCTTAAACCGAATGGAGTACATCGTATAG 3657  
Db 3971 GACACAGAGACTTGGAAAGTGCCAGAGCTTAAACCGAATGGAGTACATCGTATAG 4027

## RESULT 14

US-09-199-865-2  
; Sequence 2, Application US/09199865  
; Patent No. 6433138  
; GENERAL INFORMATION:  
; APPLICANT: Zimrin, Ann B.  
; APPLICANT: Maciag, Thomas  
; APPLICANT: Wong, Michael K.K.  
; APPLICANT: Pepper, Michael S.  
; APPLICANT: Montesano, Roberto  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS  
; FILE REFERENCE: 0036-1U1  
; CURRENT APPLICATION NUMBER: US/09/199,865  
; CURRENT FILING DATE: 1998-11-25  
; EARLIER APPLICATION NUMBER: 60/018,841  
; EARLIER FILING DATE: 1996-05-31  
; EARLIER APPLICATION NUMBER: PCT/US97/09407  
; EARLIER FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 5458  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-199-865-2

Query Match 98.8%; Score 3611.8; DB 3; Length 5458;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3613; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 39 CCTAAGCCTCTGTCGCCCTGCTCTGTGCGCTGCGAGCAAGGTGTGTGGGCGCTCGG 98  
Db 9 CCTAAGCCTCTGTCGCCCTGCTCTGTGCGCTGCGAGCAAGGTGTGTGGGCGCTCGG 68

QY 99 TCAGTTCAGGTTCGAGATCCTGTCATCGAGACGTGAACGGGGAGCTGCAGACCGGAA 158  
Db 69 TCAGTTCAGGTTCGAGATCCTGTCATCGAGACGTGAACGGGGAGCTGCAGACCGGAA 128

QY 159 CTGCTGGCGGGCGCCCGGAACCGGGAGACCGCAAGTGCACCCGCGAGGTGTGACAC 218  
Db 129 CTGCTGGCGGGCGCCCGGAACCGGGAGACCGCAAGTGCACCCGCGAGGTGTGACAC 198

QY 219 ATACTTCAAGGTGCTCAAGAGTATCATGTCGCCGTCAAGCGGGGGCGCTGAC 278  
Db 189 ATACTTCAAGGTGCTCAAGAGTATCATGTCGCCGTCAAGCGGGGGCGCTGAC 248

QY 279 CTTGGCTCAGGTTCACCGCTGTCATCGGGGCGACACCTTCAACCTCAAGCGCGCG 338  
Db 249 CTTGGCTCAGGTTCACCGCTGTCATCGGGGCGACACCTTCAACCTCAAGCGCGCG 308

QY 339 CGGCAACGACCGCAACCGCATCTGTGCTGCTTTCAGTTCGCTGCGCGAGGTCTTATAC 398  
Db 309 CGGCAACGACCGCAACCGCATCTGTGCTGCTTTCAGTTCGCTGCGCGAGGTCTTATAC 368

QY 399 GTTGTGTGGAGCGGTGGAGTTCAGTAATGACACCGTTCAACCTGACAGTATTATGA 458  
Db 369 GTTGTGTGGAGCGGTGGAGTTCAGTAATGACACCGTTCAACCTGACAGTATTATGA 428

QY 459 AAAGGCTTCTCATCGGGATGATCAACCCGCGCGAGTGGCAGCGCTGAAGCAGAA 518  
Db 429 AAAGGCTTCTCATCGGGATGATCAACCCGCGCGAGTGGCAGCGCTGAAGCAGAA 488

QY 519 CACGGGCTTTCACCTTTCAGTATCAGATCCGGGTGACCTGTGATGACTACTACTATGG 578  
Db 489 CACGGGCTTTCACCTTTCAGTATCAGATCCGGGTGACCTGTGATGACTACTACTATGG 548

QY 579 CTTTGGCTGYAATAAGTTCTGCCGCCCCAGAGATGACTTCTTTGGACACTATGCCCTGTGA 638

Db 549 CTTTGGCTGYAATAAGTTCTGCCGCCCCAGAGATGACTTCTTTGGACACTATGCCCTGTGA 608  
QY 639 CCAGAAATGGCAACAAACTTTCATGGAAGCTGATGGGGCCCGAAATGTAACAGAGCTAT 698  
Db 609 CCAGAAATGGCAACAAACTTTCATGGAAGCTGATGGGGCCCGAAATGTAACAGAGCTAT 668  
QY 699 TTGCCGACAAGGCTGCAGTCTTAAGCATGGGTCTTGCAAACTCCACAGGTGACTGCGGTG 758  
Db 669 TTGCCGACAAGGCTGCAGTCTTAAGCATGGGTCTTGCAAACTCCACAGGTGACTGCGGTG 728  
QY 759 CCAGTAYGGCTGCGAAGGCTGTACTGTGTAAGTGCATCCACACCGGGAGTGCCTCCA 818  
Db 729 CCAGTAYGGCTGCGAAGGCTGTACTGTGTAAGTGCATCCACACCGGGAGTGCCTCCA 788  
QY 819 CGGCATCTGTAATAGCCCTGGCAGTGCCTCTGTGAGACCAACTGGGGCGGCCAGCTCTG 878  
Db 789 CGGCATCTGTAATAGCCCTGGCAGTGCCTCTGTGAGACCAACTGGGGCGGCCAGCTCTG 848  
QY 879 TGACAAAGATCTCAATTTACTGTGGGACTCATACAGCGGTGTCTCAACGGGGGAACTTGTAG 938  
Db 849 TGACAAAGATCTCAATTTACTGTGGGACTCATACAGCGGTGTCTCAACGGGGGAACTTGTAG 908  
QY 939 CAACACAGGCCCTGACAAATATCAGTGTTCCTGCGCTGAGGGGTATTTACAGACCCAATG 998  
Db 909 CAACACAGGCCCTGACAAATATCAGTGTTCCTGCGCTGAGGGGTATTTACAGACCCAATG 968  
QY 999 TGAAATTTGCTGAGCAGCGCTGCTCTGATCCTGTCAACACAGAGGAGCTGTGAAGGA 1058  
Db 969 TGAAATTTGCTGAGCAGCGCTGCTCTGATCCTGTCAACACAGAGGAGCTGTGAAGGA 1028  
QY 1059 GACCTCCCTGGGCTTTGAGTGTGAGTGTTCCTCCAGGCTGCAGCGGCCCCACATGCTCTAC 1118  
Db 1029 GACCTCCCTGGGCTTTGAGTGTGAGTGTTCCTCCAGGCTGCAGCGGCCCCACATGCTCTAC 1088  
QY 1119 AAACATTTGATGACTGTTCCTTAATTAACCTGTTCCACGGGGGACCTGCCAGGACCTGGT 1178  
Db 1089 AAACATTTGATGACTGTTCCTTAATTAACCTGTTCCACGGGGGACCTGCCAGGACCTGGT 1148  
QY 1179 TAACGGAATTTAAGTGTGTGCCCCCAGAGTGCAGTGGGAAACCTGCGAGTTAGATGC 1238  
Db 1149 TAACGGAATTTAAGTGTGTGCCCCCAGAGTGCAGTGGGAAACCTGCGAGTTAGATGC 1208  
QY 1239 AAATGAATGTGAGGCCAAACCTTTGTGTAAACGCAAACTCTGTAAAGAACTCTCATTTGCCAG 1298  
Db 1209 AAATGAATGTGAGGCCAAACCTTTGTGTAAACGCAAACTCTGTAAAGAACTCTCATTTGCCAG 1268  
QY 1299 CTAATACTGGAAGTGTCTTCCCGGCTGGATGGGTCAAGATTTGACATAAATAATTAATGA 1358  
Db 1269 CTAATACTGGAAGTGTCTTCCCGGCTGGATGGGTCAAGATTTGACATAAATAATTAATGA 1328  
QY 1359 CTGCGCTTGGCGAGTGTGAGAACTGACGCTCTGTCGGGATTTGTTAATGTTATCGCTG 1418  
Db 1329 CTGCGCTTGGCGAGTGTGAGAACTGACGCTCTGTCGGGATTTGTTAATGTTATCGCTG 1388  
QY 1419 TATCTGTCCACCTGGCTATGCGAGCGCATCACTGTGAGAGAGACATCGATGAATGTGCCAG 1478  
Db 1389 TATCTGTCCACCTGGCTATGCGAGCGCATCACTGTGAGAGAGACATCGATGAATGTGCCAG 1448  
QY 1479 CAACCCCTGTTTGAATTTGGGGGTCACTGTGAGAAATGAATCAACAGATTCCAGTGTCTGTG 1538  
Db 1449 CAACCCCTGTTTGAATTTGGGGGTCACTGTGAGAAATGAATCAACAGATTCCAGTGTCTGTG 1508  
QY 1539 TCCCACTGTTTCTCTGGAAACCTCTGTCAGCTGGACATCGATTTATTTGTCAGCTTAATCC 1598  
Db 1509 TCCCACTGTTTCTCTGGAAACCTCTGTCAGCTGGACATCGATTTATTTGTCAGCTTAATCC 1568  
QY 1599 CTGCCAGAACCGGTGCCAGTGTCTAACACCGTGCAGTGAATAATTTCTGCAAGTGCCTCGA 1658  
Db 1569 CTGCCAGAACCGGTGCCAGTGTCTAACACCGTGCAGTGAATAATTTCTGCAAGTGCCTCGA 1628  
QY 1659 GGAATAAGGGCAAGAACTGTCTCAACCTGTAAGAGCACTGCGCGCAGACCCCTGTGA 1718

Db	1629	GGACTATGAGGGGCAAGAACTGCTCTCACACCTGAAAGACCACTGCGGCACGACCCCTGTGA	1688
Qy	1719	AGTGATTTGACAGCTGCGACAGTGGCCATGCGTTCCAAACGACACACCTGAAAGGGGTGGGTA	1778
Db	1689	AGTGATTTGACAGCTGCGACAGTGGCCATGCGTTCCAAACGACACACCTGAAAGGGGTGGGTA	1748
Qy	1779	TATTTCTCTCAACCGTCTGTGGTCTCACGGGAAGTGCAGAGTCAGTTCGGGAGGCAAAATT	1838
Db	1749	TATTTCTCTCAACCGTCTGTGGTCTCACGGGAAGTGCAGAGTCAGTTCGGGAGGCAAAATT	1808
Qy	1839	CACCTGTGACTGTAAACAAAGGCTTCACGGGAACATACTGCGCATGAAATATTAATGACTG	1898
Db	1809	CACCTGTGACTGTAAACAAAGGCTTCACGGGAACATACTGCGCATGAAATATTAATGACTG	1868
Qy	1899	TGAGAGCAACCCCTTGTAAGAAACGGTGGCACTTGCATCGATGGTGTCAACTCCCTACAAGTG	1958
Db	1869	TGAGAGCAACCCCTTGTAAGAAACGGTGGCACTTGCATCGATGGTGTCAACTCCCTACAAGTG	1928
Qy	1959	CATCTGTAGTGACCGCTGGGAGGGGGCTACTGTGAAACCAATATTAATGACTGCGAGCCA	2018
Db	1929	CATCTGTAGTGACCGCTGGGAGGGGGCTACTGTGAAACCAATATTAATGACTGCGAGCCA	1988
Qy	2019	GAACCCCTGCCAAATGGGGGACGTGTGGGACCTGGTCAATGACTTCTACTGTGACTG	2078
Db	1989	GAACCCCTGCCAAATGGGGGACGTGTGGGACCTGGTCAATGACTTCTACTGTGACTG	2048
Qy	2079	TAAAAATGGGTGGAAAGGAAAGACCTGCCACTACAGTGCACAGTCAGTGTGATGAGGCCAC	2138
Db	2049	TAAAAATGGGTGGAAAGGAAAGACCTGCCACTACAGTGCACAGTCAGTGTGATGAGGCCAC	2108
Qy	2139	GTGCAACAAACCGGTGGCACCTGCTATGATGAGGGGGATGCTTTTAAGTGCATGTGTCTGTG	2198
Db	2109	GTGCAACAAACCGGTGGCACCTGCTATGATGAGGGGGATGCTTTTAAGTGCATGTGTCTGTG	2168
Qy	2199	CGGCTGGGAAGAAACAACCTGTGTAAATAGATGAGGGGGATGCTTTTAAGTGCATGTGTCTGTG	2258
Db	2169	CGGCTGGGAAGAAACAACCTGTGTAAATAGATGAGGGGGATGCTTTTAAGTGCATGTGTCTGTG	2228
Qy	2259	CCATAATGGGGGGACATGTGTGTCACAGCGGAGTCTTTTACGTGCGCTGTGCAAGGAAGG	2318
Db	2229	CCATAATGGGGGGACATGTGTGTCACAGCGGAGTCTTTTACGTGCGCTGTGCAAGGAAGG	2288
Qy	2319	CTGGGAGGGGCCACTCTGTGCTCAGAAATACCAATGACTGCAGCGCCCTCATCCCTGTTACAA	2378
Db	2289	CTGGGAGGGGCCACTCTGTGCTCAGAAATACCAATGACTGCAGCGCCCTCATCCCTGTTACAA	2348
Qy	2379	CAGCGGCACCTGTGTGGATGAGACAACATGTGTAACGGTGCAGATGTGCGCCCGGGTTTTCG	2438
Db	2349	CAGCGGCACCTGTGTGGATGAGACAACATGTGTAACGGTGCAGATGTGCGCCCGGGTTTTCG	2408
Qy	2439	TGGGCCCGACCTGCAGATTAACATGATGCGAGTCTTCACTTGTGCGCTTTGGAGC	2498
Db	2409	TGGGCCCGACCTGCAGATTAACATGATGCGAGTCTTCACTTGTGCGCTTTGGAGC	2468
Qy	2499	GACCTGTGTGATGAGATCAATGGCTACCGGTGTGTGCGCCTCCAGGGGCACAGTGGTGC	2558
Db	2469	GACCTGTGTGATGAGATCAATGGCTACCGGTGTGTGCGCCTCCAGGGGCACAGTGGTGC	2528
Qy	2559	CAAGTGCCAGGAAGTTTCAGGGAGACCTTGTGCATCAACATGGGGAGTGTGATACAGATGG	2618
Db	2529	CAAGTGCCAGGAAGTTTCAGGGAGACCTTGTGCATCAACATGGGGAGTGTGATACAGATGG	2588
Qy	2619	GGCCAAATGGGAATGATGACTGTAACTGCGCAGTGTGATGCGGAGTGTGATGCGCTGCTC	2678
Db	2589	GGCCAAATGGGAATGATGACTGTAACTGCGCAGTGTGATGCGGAGTGTGATGCGCTGCTC	2648
Qy	2679	AAAGGTCTGTGTGTGGCCCTCGACCTTGTGCTGTCTCCAAAGGGGCACAGCGAGTCCCCCAG	2738
Db	2649	AAAGGTCTGTGTGTGGCCCTCGACCTTGTGCTGTCTCCAAAGGGGCACAGCGAGTCCCCCAG	2708
Qy	2739	CGGGCAGAGCTGCATCCCCATCTCTGGACGAACAAGTGTTCGTTCACACCCCTGCACTGTGTGT	2798
Db	2709	CGGGCAGAGCTGCATCCCCATCTCTGGACGAACAAGTGTTCGTTCACACCCCTGCACTGTGTGT	2768

Qy	2799	GGGCGAGTGTCCGTCCTTCAGTCTCTCAGCCGGTGAAGACAAAGTGCACCTCTGACTCCCTA	2855
Db	2769	GGGCGAGTGTCCGTCCTTCAGTCTCTCAGCCGGTGAAGACAAAGTGCACCTCTGACTCCCTA	2828
Qy	2859	TTACGAGATAACTGTGCGAAATCAATTTACCTTTAAACAAGGAGATGATGTCAACAGG	2918
Db	2829	TTACGAGATAACTGTGCGAAATCAATTTACCTTTAAACAAGGAGATGATGTCAACAGG	2888
Qy	2919	TCCTTACCGGAGACATTTGCGAGTGAATTTGAGGAATTTGAAATATTTTGAAGAAATGTTTC	2978
Db	2889	TCCTTACCGGAGACATTTGCGAGTGAATTTGAGGAATTTGAAATATTTTGAAGAAATGTTTC	2948
Qy	2979	CGCTGAATATTTCAATCTACATCGCTTCGAGCGCTTCCCTTTACGCGAAACAATGAAATACA	3038
Db	2949	CGCTGAATATTTCAATCTACATCGCTTCGAGCGCTTCCCTTTACGCGAAACAATGAAATACA	3008
Qy	3039	TGTGGCCATTTCTGCTGAAGATATACGGGATGATGGGAACCCGATCAAGGAAATCACTGA	3098
Db	3009	TGTGGCCATTTCTGCTGAAGATATACGGGATGATGGGAACCCGATCAAGGAAATCACTGA	3068
Qy	3099	CAAAATTAATCGATCTTGTAGTAAACGTGATGAAACAGCTCCGCTGATCTGCCGTTCG	3158
Db	3069	CAAAATTAATCGATCTTGTAGTAAACGTGATGAAACAGCTCCGCTGATCTGCCGTTCG	3128
Qy	3159	AGAAATTAAGAGTTTCAGAGCGCGCTCTGGAAGAAACAGAAACAGATTTCCCTGTTCCCTTGCT	3218
Db	3129	AGAAATTAAGAGTTTCAGAGCGCGCTCTGGAAGAAACAGAAACAGATTTCCCTGTTCCCTTGCT	3188
Qy	3219	GAGCTCTGTCTTAACTGTGGCTTGATCTGTGTTGGTGAAGCCCTTTACTTGGTGCTCT	3278
Db	3189	GAGCTCTGTCTTAACTGTGGCTTGATCTGTGTTGGTGAAGCCCTTTACTTGGTGCTCT	3248
Qy	3279	GCGAAGCGGCGGAAGCCGGCAGCCACACACTCAGCTCTTGAGGACAAACACACACAA	3338
Db	3249	GCGAAGCGGCGGAAGCCGGCAGCCACACACTCAGCTCTTGAGGACAAACACACACAA	3308
Qy	3339	CAACGTGCGGAGCAGCTGAAACAGATCAAAAAACCCCATTTGAGAAAACATGGGGCCAAACAC	3398
Db	3309	CAACGTGCGGAGCAGCTGAAACAGATCAAAAAACCCCATTTGAGAAAACATGGGGCCAAACAC	3368
Qy	3399	GGTCCCATCAAGATTTACGGAGACAGAACTCCAAAATGCTTAAATAATAGGACACACAA	3458
Db	3369	GGTCCCATCAAGATTTACGGAGACAGAACTCCAAAATGCTTAAATAATAGGACACACAA	3428
Qy	3459	TTCTGAAGTAGAAGGAGCGCATGGAACAAACACGACAGAAAGCCCGGTTTGGCAAGCA	3518
Db	3429	TTCTGAAGTAGAAGGAGCGCATGGAACAAACACGACAGAAAGCCCGGTTTGGCAAGCA	3488
Qy	3519	GCCGGCGTATACGCTGTGTAGACAGAGAAGAGAGCCGCCACCGGACGCGGACAAACAA	3578
Db	3489	GCCGGCGTATACGCTGTGTGTAGACAGAGAAGAGAGCCGCCACCGGACGCGGACAAACAA	3548
Qy	3579	CCCAAACTGGACAAACAAACAGGACAAACAGAGACTTGGAAAGTCCCGCAGAGCTTTAAACCG	3638
Db	3549	CCCAAACTGGACAAACAAACAGGACAAACAGAGACTTGGAAAGTCCCGCAGAGCTTTAAACCG	3608
Qy	3639	AATGGAGTACATCGTATAG	3657
Db	3609	AATGGAGTACATCGTATAG	3627

## RESULT 15

; Sequence 2, Application US/10213329  
 ; Patent No. 6825007  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zimrin, Ann B.  
 ; APPLICANT: Maciag, Thomas  
 ; APPLICANT: Wong, Michael K.K.  
 ; APPLICANT: Pepper, Michael S.  
 ; APPLICANT: Montesano, Roberto  
 ; TITLE OF INVENTION: THERAPEUTIC AND COMPOSITIONS



**TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NICI.ETC ACIDS**

[illegible]

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Query Match          98.8%; Score 3611.8; DB 3; Length 5458;
Best Local Similarity 99.8%; Pred. NO. 0;
Matches 3613; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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Qy	39	CCTAAGCCTCTCTGCTCGCCCTGCTCTGTGTCCTCGGAGCCAAAGTGTGTGTGGGCGCTCGGG	98
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Qy	99	TCAGTTCCGAGTTGAGATCCTGTCCATCAGAAAGTGAACGGGAGCTGCAGAACGGGAA	158
Db	69	TCAGTTCCGAGTTGAGATCCTGTCCATCAGAAAGTGAACGGGAGCTGCAGAACGGGAA	128
Qy	159	CTGCTGGGGCGGCCCGGGAAACCGGGAGACCGCAAGTGCAACCGCGCAGCAGTGTGCAC	218
Db	129	CTGCTGGGGCGGCCCGGGAAACCGGGAGACCGCAAGTGCAACCGCGCAGCAGTGTGCAC	188
Qy	219	ATACTTCAAAGTGTGCCTCAAGGAGTATCAGTCCGCGTCACGCGCGGGGGGCCCTCGAG	278
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Qy	279	CTTCGGGCTCAGGGTCCACGCGTGCATCGGGGGCAACACCTTCAACCTCAAGGCCAGCCG	338
Db	249	CTTCGGGCTCAGGGTCCACGCGTGCATCGGGGGCAACACCTTCAACCTCAAGGCCAGCCG	308
Qy	339	CGGCAACGACCGCAACCGCATCGTGTGCCTTTCAGTTTCGCCCTGGCGCAGCTCTATAC	398
Db	309	CGGCAACGACCGCAACCGCATCGTGTGCCTTTCAGTTTCGCCCTGGCGCAGCTCTATAC	368
Qy	399	GTTGCTTGTGGAGCGTGGGATTCAGTAATGACAACCTTCAACCTGACAGTATTAATGA	458
Db	369	GTTGCTTGTGGAGCGTGGGATTCAGTAATGACAACCTTCAACCTGACAGTATTAATGA	428
Qy	459	AAAGGCTTCTCAGTCGGGCATGATCAACCCAGCCGCGTGGCAGACGCTGAAGCAGAA	518
Db	429	AAAGGCTTCTCAGTCGGGCATGATCAACCCAGCCGCGTGGCAGACGCTGAAGCAGAA	488
Qy	519	CACGGCGTTGCCCACTTTGAGTATCAGATCCGCGTGACCTGTGATGACTACTACTATGG	578
Db	489	CACGGCGTTGCCCACTTTGAGTATCAGATCCGCGTGACCTGTGATGACTACTACTATGG	548
Qy	579	CTTTGGCTGYAATAAGTTCTTCCGCCCCOAGAGATGACTTTCTTTGGACAATATGCTGTGA	638
Db	549	CTTTGGCTGYAATAAGTTCTTCCGCCCCOAGAGATGACTTTCTTTGGACAATATGCTGTGA	608
Qy	639	CCAGATGGCAACAAAACCTTCATGGAGGCTGGATGGGCCCGCAATGTAAACAGAGCTAT	698
Db	609	CCAGATGGCAACAAAACCTTCATGGAGGCTGGATGGGCCCGCAATGTAAACAGAGCTAT	668
Qy	699	TTGCCGACAAGGCTGCAGTCTTAAGCATGGGTCTTTGCAAACTCCAGGTCAGCTCAGGTG	758
Db	669	TTGCCGACAAGGCTGCAGTCTTAAGCATGGGTCTTTGCAAACTCCAGGTCAGCTCAGGTG	728
Qy	759	CCAGTAYGGCTGGCAAGCGCTGTACTGTGATAAGTGCATCCCAACCCGGATGCGTCCA	818
Db	729	CCAGTAYGGCTGGCAAGCGCTGTACTGTGATAAGTGCATCCCAACCCGGATGCGTCCA	788



QY	1899	TGAGAGCAACCCCTTGTAGAAA	CGGTGGCACTTGCATCGATGGTGTCAA	CTCCTACAAGTG	1958
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QY	1869	TGAGAGCAACCCCTTGTAGAAA	CGGTGGCACTTGCATCGATGGTGTCAA	CTCCTACAAGTG	1928
Db					
QY	1959	CATCTGTAGTACGGCTGGAGGGG	CGCTTACTGTGAAACCAATTAAT	TAAATGACTGCAAGCCA	2018
Db					
QY	1929	CATCTGTAGTACGGCTGGAGGGG	CGCTTACTGTGAAACCAATTAAT	TAAATGACTGCAAGCCA	1988
Db					
QY	2019	GAACCCCTGCCACAAATGGGGG	CGATGTCGGACCTGGTCAATGAC	TTCTTACTGTGACTG	2078
Db					
QY	1989	GAACCCCTGCCACAAATGGGGG	CGATGTCGGACCTGGTCAATGAC	TTCTTACTGTGACTG	2048
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QY	2079	TAAAAATGGGTGGAAGAGAA	AGACCTGCCACTCAAGTGACAGT	CAGTGTGATGAGGCCAC	2138
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QY	2049	TAAAAATGGGTGGAAGAGAA	AGACCTGCCACTCAAGTGACAGT	CAGTGTGATGAGGCCAC	2108
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QY	2139	GTGCAACAAACGGTGGCA	CCCTGCTATGATGAGGGGGAT	GGCTTTTAAAGTGCAATGTCTGTGG	2198
Db					
QY	2109	GTGCAACAAACGGTGGCA	CCCTGCTATGATGAGGGGGAT	GGCTTTTAAAGTGCAATGTCTGTGG	2168
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QY	2199	CGGCTGGGAAGGAACA	CCCTGTAAACATAGCCCGAAACAGT	AGCTGCCCTGCCAACCCCTG	2258
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QY	2169	CGGCTGGGAAGGAACA	CCCTGTAAACATAGCCCGAAACAGT	AGCTGCCCTGCCAACCCCTG	2228
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QY	2259	CCATAATGGGGGCA	CATGTGTGGTCAACGGCGAGT	CTCTTACGTGGCGTCTGCAAGGAAGG	2318
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QY	2229	CCATAATGGGGGCA	CATGTGTGGTCAACGGCGAGT	CTCTTACGTGGCGTCTGCAAGGAAGG	2288
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QY	2319	CTGGAGGGGCCCATCTGT	GCTCAGAAATACCAATGACT	CAGAGCCCTCATCCCTGTATCAA	2378
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QY	2389	CTGGAGGGGCCCATCTGT	GCTCAGAAATACCAATGACT	CAGAGCCCTCATCCCTGTATCAA	2348
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QY	2379	CAGCGGACCTGTGTGAT	TGGAGACAACCTGTGACCGGT	GGCAATGTGCCCGGGTTTGC	2438
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QY	2349	CAGCGGACCTGTGTGAT	TGGAGACAACCTGTGACCGGT	GGCAATGTGCCCGGGTTTGC	2408
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QY	2499	GACCTGTGTGATGAGAT	CAATGGCTACCGGTGTGCT	CGCCCTCCAGGGCACAGTGGTGC	2558
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QY	2469	GACCTGTGTGATGAGAT	CAATGGCTACCGGTGTGCT	CGCCCTCCAGGGCACAGTGGTGC	2528
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QY	2589	GGCCAAATGGGATGAT	GACTGTAATACCTGCCAGT	GCTGTAATGGACGGATCGCCTGCTC	2648
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QY	2679	AAAGGTCTGTGTGGCCCT	CGACCTTGCCTCCAAAGGG	CACAGCGAGTGCCTCCAG	2738
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QY	2739	CGGCGAGCTGCAATCCC	CCATCTGGAGCAGCAGT	GTCTTGGTCCACCCCTGCATGGTGT	2798
Db					
QY	2709	CGGCGAGCTGCAATCCC	CCATCTGGAGCAGCAGT	GTCTTGGTCCACCCCTGCATGGTGT	2768
Db					
QY	2799	GGGCGAGTGTGGTCTT	CCAGTCTCCAGCCGGTGAAG	CAAGTGCACTCTGACTCCTA	2858
Db					
QY	2769	GGGCGAGTGTGGTCTT	CCAGTCTCCAGCCGGTGAAG	CAAGTGCACTCTGACTCCTA	2828
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QY	2859	TTACCAGGATAACTGT	GCGAACATCACATTTTAC	CTTTTAAAGGAGATGATGTCA	2918
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QY	2829	TTACCAGGATAACTGT	GCGAACATCACATTTTAC	CTTTTAAAGGAGATGATGTCA	2888
Db					
QY	2919	TCCTTACTACGAGCA	CAATTTGAGGAATTTGAA	TATTTTGAAGAATGTTTC	2978
Db					
QY	2889	TCCTTACTACGAGCA	CAATTTGAGGAATTTGAA	TATTTTGAAGAATGTTTC	2948
Db					
QY	2979	CGCTGAATATTTCAAT	CTACATCGCTTGGAGCCT	TTCCCTTTCAGCGAACAAATGA	3038
Db					

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Job time : 653 secs

Db	2949	CGCTGAATATTTCAAT	CTACATCGCTTGCAGCCT	TTCCCTTTCAGCGAACAAATGA	3008
QY					
QY	3039	TGTGGCCATTTTCTGCT	TGAAGATATACGGGAT	TATACGGGAAACCCGATCA	3098
Db					
QY	3009	TGTGGCCATTTTCTGCT	TGAAGATATACGGGAT	TATACGGGAAACCCGATCA	3068
Db					
QY	3099	CAAAATAATCGATCTT	GTAGTAAACGTCATGGAA	ACAGCTCGCTGATTTGCTG	3158
Db					
QY	3069	CAAAATAATCGATCTT	GTAGTAAACGTCATGGAA	ACAGCTCGCTGATTTGCTG	3128
Db					
QY	3159	AGAAGTAAAGATTTCA	GAGCGGCTCTGAAGAA	CAGAAACAGATTTTCTG	3218
Db					
QY	3129	AGAAGTAAAGATTTCA	GAGCGGCTCTGAAGAA	CAGAAACAGATTTTCTG	3188
Db					
QY	3219	GAGCTCTGTCTTAA	CTGTGCTTGGATCTGTT	GTGTTGAGCGGCTTCTAC	3278
Db					
QY	3189	GAGCTCTGTCTTAA	CTGTGCTTGGATCTGTT	GTGTTGAGCGGCTTCTAC	3248
Db					
QY	3279	GCGGAAGCGCGGAAG	CCGGAGCCACACACTCAG	CCCTCTTGAGGACAAACCA	3338
Db					
QY	3249	GCGGAAGCGCGGAAG	CCGGAGCCACACACTCAG	CCCTCTTGAGGACAAACCA	3308
Db					
QY	3339	CAAACGTGCGGGAGC	AGCTGAAACAGATCAAAA	CCCCCATTTGAGAAACAT	3398
Db					
QY	3309	CAAACGTGCGGGAGC	AGCTGAAACAGATCAAAA	CCCCCATTTGAGAAACAT	3368
Db					
QY	3399	GGTCCCATCATCAGG	ATTACGGAACCAAGAACT	CCAAAATGTCTAAAAT	3458
Db					
QY	3369	GGTCCCATCATCAGG	ATTACGGAACCAAGAACT	CCAAAATGTCTAAAAT	3428
Db					
QY	3459	TTCTGAAGTAGAAG	AGAGGACGACATGGACA	AAACACCGCGTTTTGGCA	3518
Db					
QY	3429	TTCTGAAGTAGAAG	AGAGGACGACATGGACA	AAACACCGCGTTTTGGCA	3488
Db					
QY	3519	GCCGGCGTATACGCT	GTAGACAGAGAAGAA	AGCCCCCAACGGCAC	3578
Db					
QY	3489	GCCGGCGTATACGCT	GTAGACAGAGAAGAA	AGCCCCCAACGGCAC	3548
Db					
QY	3579	CCCAAACTGGACAA	CAAAACAGGACCAACAG	AGACTTTGGAAGTGGCC	3638
Db					
QY	3549	CCCAAACTGGACAA	CAAAACAGGACCAACAG	AGACTTTGGAAGTGGCC	3608
Db					
QY	3639	AATGGAGTACATCGT	TATAG 3657		
Db					
QY	3609	AATGGAGTACATCGT	TATAG 3627		
Db					